

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run On: February 9, 2000, 11:00:06 ; Search time 5690.77 Seconds
(without alignments)
10309.021 Million cell updates/sec

Title: US-09-190-246-1

Perfect score: 15538

Sequence: 1 tcgcggtttcgtgatgcac.....tatcacgagggcccttctgc 15538

Scoring table: IDENTITY_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:

Word size : 0

Number of hits that pass the threshold : 9077268

1: em_est1:*
2: em_est2:*
3: em_est3:*
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5: em_est5:*
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7: em_est7:*
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9: em_est9:*
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105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	720	4.6	954	61	AL044364
2	716.2	4.6	1067	74	AU081137
3	688	4.4	1089	74	AU081137
c	679.4	4.4	757	88	AQ856202
5	626.2	4.0	734	64	AL039459
6	620	4.0	718	79	AG010489
c	604.2	3.9	784	88	AQ876119
					AL044364 DKFp434C
					AU081137 AU081137
					AU081124 AU081124
					AQ856202 nbe0001F
					AL039459 DKFp434C
					AG010489 Homo sapi
					AQ876119 V133E1 mt

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Db	155	ATTAAAAATGAAGTTTAAAAATCAATCTAAGTATATATATGAGTAAACTTGGTCTGACGTT	96
QY	14049	accaatgcttaatcagtgaggcgaacctatctcagcgatctctgtctatttggttcaac	14104
Db	95	ACCAATGCTTAATCAGTGAGCGACCTATCTCAGCGATCTGTCTATTTCGTTCACTCC	40
RESULT	5		
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LOCUS			
DEFINITION	AL039459	734 bp	mrna
ACCESSION	DFXPp43401210.51	434 (synonym: htes3)	Homo sapiens
VERSION	DFXPp43401210.3		EST
KEYWORDS	AL039459.2	GI:5935158	29-SEP-1999
SOURCE	EST		Homo sapiens
ORGANISM	human.		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann, S.		
JOURNAL	EST (Duesterhoeft, et al.)		
COMMENT	Unpublished (1999).		
	On Jul 7, 1999 this sequence version replaced gi:5408507.		
	Contact: Duesterhoeft A		
	MFPS		
	Am Klopferspitz 18a D-82152 Martinsried, Germany		
	This is the 3' sequence of the clone insert		
	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;		
	sequenced by Qiagen within the cDNA sequencing consortium of the German Genome Project.		
	No RI sequence available.		
	This clone is available at the RZPD in Berlin.		
	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.		
FEATURES			
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	/dev_stage="adult"		
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	/note="vector: pSport1; Site_1: 199 c 194 g 161 t 8 Others		
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Matches	688;	Conservative	0; Mismatches 30; Indels 8; Gaps 4
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/	13191	ggttatccacagatacaggggataacgcaggaagaatacgtgagcaaaaggccagcaaa	13250
69	69	GCTTATCCAGAGTAATCAGGGGATAACGACGAGGAAGAACATGTGAGCAAAAGGCCACAA	128
/	13251	agggcaggaaccgtataaaggcggtgtgctgagctttttccataggtccgcgccctg	13310
129	129	AGGCAGGAACCTTAAAGAGGCGGGTTCGTGGCGTTTTCCTATAGGCTCGGCCCTG	188
/	13311	acgagcatcaaaaaatcgacgtcaagtcaggtggcgaaacccgacagactataa	13370
189	189	ACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACATAAA	248

QY	13371	gataccagcggtttccccctggaaagcctcccctgcgtgcacctcttcctgaccacccctgcgc						13430
Db	249	GATACAGCGGTTCCTCCCTGGAGACTCCTCTGCTGCCTTCTCTTGTTTCCGACCCTGCCG						308
QY	13431	ttaccggatcacctgtccgccttctcccttccttggaagcgtggcgcttctcatagtctaac						13490
Db	309	TTACCGGATACCTGTGCCGCCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAC						368
QY	13491	gctgtagttatctcagttcgggtgttagtgttcgttcgctccaagctggcgctgtgtgcagaac						13550
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Db	609	ACAGTATTTTGGTATCTGCGCTCTGCTGAACACAGTTTACCTTCGGA AAAAANGTGGGT						668
QY	13787	agctcttg----atccggcaaaaacacccgcgtggtgcggtgtttttgtttgtaa						13842
Db	669	AGNC TTGGATCGCGNAAA AAAAACCAACCGCTGGTTAGNGTGTGTTTTTTNTTNC						728
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DEFINITION	Homo sapiens genomic DNA, 21q region, clone: P7H8X25, genomic survey sequence.	718 bp	DNA	GSS	14-APR-1999			
ACCESSION	AG010489							
VERSION	AG010489.1							
KEYWORDS	GSS:							
SOURCE	Homo sapiens							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
AUTHORS	Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.							
JOURNAL	Homo sapiens genomic DNA, chromosome 21q							
REFERENCE	Published Only in Database (1998) In press							
AUTHORS	Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.							
TITLE	Direct Submission							
JOURNAL	Submitted (16-JUL-1998) to the DDBJ/EMBL/GenBank databases.							
COMMENT	Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hatoric@nc.ims.u-tokyo.ac.jp. Tel:0427-78-9732, Fax:0427-78-9561)							
FEATURES	On Feb 5, 1999 this sequence version replaced gi:2789511. AG004363; Submitted-(17-Jan-1998).							
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	/map="21q"							
BASE COUNT	176 a 191 c 187 g 158 t							6 others
ORIGIN								

Gene Disruption Unpublished (1999) Contact: Kumar A Michael Snyder, Dept. of Mol. Cell. and Dev. Biology Yale University P.O. Box 208103, New Haven, CT 06520-8103, USA Tel: 203 432 9949 Fax: 203 432 6161 Email: anuj.kumar@yale.edu te of min-3xHA/lacZ insertion. Seq primer: GGCTTCCTTCCTTTGGAGTAC Class: transposon-tagged. Location/Qualifiers 1. 784									
/organism="Saccharomyces cerevisiae" /strain="Y2278 - S288C background, cir(0) rho(0)" /db_xref="taxon:4932" /clone_lib="min-3xHA/lacZ Insertion Library, strain Y2278" /lab_host="E. coli" /note="vector: pHS56-Sal; A yeast genomic DNA library without 2 micron or mitochondrial DNA was prepared in pHS56-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a min-3xHA/lacZ mini-transposon containing lacZ, URA3, and tet resistance."									
FEATURES source									
BASE COUNT 187 a 200 c 210 g 186 t 1 others									
ORIGIN									
Query Match 3.9%; Score 604.2; DB 88; Length 784; Best Local Similarity 97.8%; Pred. No. 1.9e-109; Matches 612; Conservative 0; Mismatches 14; Indels 0; Gaps 0;									
QY	13276	gttctggggtttttccataggtccgcccccttcacagagatcaaaaaatcgacgtc	13335						
DB	784	GGTGTGGCTTTTTCATAGGCTCGGCCCTTGTACGAGCATCAAAAATCGAGCTC	725						
QY	13336	aagtcagagtgccgaacccagagactataaagataccagggtttccccctggaaag	13395						
DB	724	AAGTCAGAGTGGCGAAACCCGACAGACTATAAAGATCCAGCGGTTTCCGCCGGAAG	665						
QY	13396	ctccctcgtcgctctcctgttccgacctgcgcgttacggataacctgtccgcttct	13455						
DB	664	CTCCCTCGTGGCTCTCCTGTTCGGACCTTGTCTTACCGAATACCTGTACGCCGTCT	605						
QY	13456	cccttcgggaagcgtggcgctttctcatagctcacgctgtagttatctcagttcgggtga	13515						
DB	604	CCCTTCGGAAGCGTGGCGCTTTATCATAGCTCACGCTGTAGTATCTCAGTTCGGTGTA	545						
QY	13516	ggtcgttcgctccaagctgggctgtgtgcagaaaccccccttcagccgacctgcgc	13575						
DB	544	GGTGTTCGCTCCAAAGCTGGGCTGTGTGCAGAACCCCTCGGTTACGCCACCGTGGCG	485						
QY	13576	cttatccggttaactatcgttttgatgccaacccggttaagcacgacttatcgccactggc	13635						
DB	484	CTTATCCGTAATCTATCTCTTGTAGTCCACCCCGGTAAAGACACTTATCGCCACTGGC	425						
QY	13636	agcagccactgtaacagattagcagagcgaggtatgtaggcggtgtctacagattctt	13695						
DB	424	AGCAGCCACTGGTAACAGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTT	365						
QY	13696	gaagtgtggccctaactacgctacactagaagaacagattttgtatctcgtctcgt	13755						
DB	364	GAAGTGGTGGCTTAATCTAGCGCTACACTAGAGGACAGATTGTGGTATCTCGCTCTGCT	305						
QY	13756	gaagcagattacttcggaagaggttgtagctcttgcggaacaaacacacacgcgc	13815						
DB	304	GAAGCAGATTACTTCGGAAAAAGATTGGTAGTCTTGTATCCGGCAAAACAAACACCGC	245						
QY	13816	tgttagcgtgtgtttttttgtttgtttgaagcagcagattacgcacaaaaaaggatctca	13875						
DB	244	TGTTAGCGGTGGT	185						
RESULT 7									
LOCUS AQ876119 784 bp DNA GSS 08-NOV-1999									
DEFINITION V133E1 min-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', genomic survey sequence.									
ACCESSION AQ876119									
VERSION AQ876119.1 GI:6288363									
KEYWORDS GSS.									
SOURCE baker's yeast.									
ORGANISM Saccharomyces cerevisiae									
Eukaryota; Fungi; Ascomycota; Saccharomycetales;									
Saccharomycetaceae; Saccharomycetes.									
REFERENCE 1 (bases 1 to 784)									
AUTHORS Ross-Macdonald,P., Roemer,T., Coelho,P.S.R., Agarwal,S., Kumar,A.,									
desEtages,S.A., Cheung,K.-H., Sheehan,A., Symoniatis,D., Jansen,R.,									
Umansky,L., Heldman,M., Nelson,K., Iwasaki,H., Kanada,D., Lugo,R.,									
Hager,K., Miller,P., Roeder,G.S. and Snyder,M.									
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and									
TITLE									

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Matches 604; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 13293 ataggctcgcccccctgacgagatcacaataatcagctcaagtacagagtgccgaa 13352
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Db 735 ACCGACAGACTATAAAGATCCAGGCGTTTCCCTTGGAGCTCCCTCGTGCCTCTC 676
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QY 13413 ctgttcgaccctgcccgttacggatacctgtccgcttcttccttcctgggaagcgtgg 13472
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Db 675 CTGTTCGACCCCTCGCGTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAACGGTGG 616
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QY 13473 cgctttctatagctcaagctgtagtactcagttcgtgtgagtgctgctccaaagc 13532
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Db 615 CGCTTTCTCATAGTCAAGCTGTAGTATCTCAAGTTCGCTGAGTTCGCTCCAGC 556
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QY 13533 tgggctgtgacgaaccccccttcagcccgaccgctgccccttatccggttaactatc 13592
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QY 13593 gtcttgagtcacacccggttaagacacgacttatccgactggcagcagccactggtaaca 13652
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QY 13713 acggctacactagaagaacagatattggtatctgctgctgctgaagccagttacctcg 13772
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QY 13773 gaaaagattggtagctctgacccgcaacaaacacacgcgtggtgagcgtggtttt 13832
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Db 315 GAAAAGAGTTGGTAGCTTCTTGATCCGCGCAACAAACACCGCTGGTAGCGGTGGTTTT 256
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QY 13833 ttgtttgcaagcagcagatattacgcgcagaaaaaaggatctcaagaagatcctttgatct 13892
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Db 255 TTGTTGAAGCAGCAGATATTAGCGCAGAAAAAAGGATCTCAAGAGATCCTTTGATCT 196
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QY 13893 ttctacgg 13901
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Db 195 TTCTACTG 187
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RESULT 10
AL042334 630 bp mRNA EST 29-SEP-1999
LOCUS DKFZp434O0520.s1.434 (synonym: htes3) Homo sapiens cDNA clone
DEFINITION DKFZp434O0520.3', mRNA sequence.

ACCESSION AL042334
VERSION AL042334.1 GI:5421674
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 630)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Ottenwaelder, et al.)
Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:1135177.
Contact: Ottenwaelder B

TITLE EST
JOURNAL Unpublished (1999)
COMMENT On Dec 20, 1995 this sequence version replaced gi:1135177.

MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkz-heidelberg.de;
sequenced by MediGenomix within the cDNA sequencing consortium of
the German Genome Project.

rl sequence also available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
1. .630
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/notes="Vector: pSport1; Site_1: NotI; Site_2: SalI"

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ORIGIN

Query Match 3.8%; Score 595.2; DB 61; Length 630;
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Matches 622; Conservative 0; Mismatches 8;

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Db 1 GGTATACGGTTATCCACAGATCAGGGGATACGCAGGAGAAAGAACATGTGACAAAGG 60
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QY 13243 ccagcaaaagccaggaacccgtaaaaagcgccgtgctgctgctgttttccataggtccg 13302
Db 61 CCAGCAAAAGCCAGGAAACCGTAAAAAGCGCGCTTCTCGCGCTTCTCATAGGCTCCG 120
|||||

QY 13303 ccccttgacagatcacaaaaatcacgctcaagtcagagtggtggaaacccgacag 13362
Db 121 CCCCCCTCAGCAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAACCAGCAGG 180
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QY 13363 actataaagataccagcggttttccccctggaagctccctgctgctctctgttccgac 13422
Db 181 ACTATAAGATACACAGCGTTTCCCTCGAAGCTCCCTCGTGGCTCTCTCTGTCGAC 240
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QY 13423 cctgcgcttacccgataccctgctccgcttccctccggaagcgtggcgctttctca 13482
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QY 13483 tagctcacgtgtagttatctcagttcgtggttagctgctccagcgtggcgctgct 13542
Db 301 TAGCTCACGCTGTAGTATCTCAGTTCGCTGAGTTCGCTCGCTCCAAAGCTGGGCTGT 360
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QY 13543 gaacgaaccccccttcagccgacgcgtgccccttatccggttaactatgctttagtc 13602
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QY 13603 caaccggtaagacacgacttatcgccactggcagcagccactggttaacagattagcag 13662
Db 421 CAACCCGGTAAAGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG 480
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QY 13663 agcagaggtatgtaggcgtgctacagagttcttgagtggtgcttaactacggtctaac 13722
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QY 13723 tagaagaacagtttggttatctgctctgctgaagcaggttaccttcggaagaaagct 13782
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QY 13783 tggtagctcttgatccggaacaaacaccg 13814
Db 599 TGGTAGCTCTTGATCCGGTAAACAAACACCCG 630
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RESULT 11
AL044413 615 bp mRNA EST 29-SEP-1999
LOCUS DKFZp434E172.s1.434 (synonym: htes3) Homo sapiens cDNA clone
DEFINITION DKFZp434E172.3', mRNA sequence.
ACCESSION AL044413

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VERSION      AL044413.1  GI:5432635
KEYWORDS
SOURCE
ORGANISM      human.
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS       1 (bases 1 to 615)
              Ansonge,W., Benes,V., Krieger,S., Mewes,H.W., Gassenhuber,J. and
              Wiemann,S.
TITLE         EST (Ansonge, Benes, et al.)
JOURNAL       Unpublished (1999)
COMMENT       On Dec 20, 1995 this sequence version replaced gi:1135425.
              MIPS
              Am Klopferspitz 18a D-92152 Martinsried, Germany
              This is the 3' sequence of the clone insert
              Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
              Research Center (DFKZ); Email s.wiemann@dkfz-heidelberg.de;
              sequenced by EMBL within the cDNA sequencing consortium of the
              German Genome Project.
              No r1 sequence available.
              This clone is available at the RZPD in Berlin.
              Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
              Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
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QY 13276 gttctggcggttttccataggtctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 13335
D 61 GTGCTGGCGGTTTTCATAGGCTCGCGCCCTGACGAGCATCACAAATCGACGCTC 120
QY 13336 aagtcagaggtggcgaacccagacaggaactataagataccagcggtttcccccctggaag 13395
D 121 AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACACAGCGTTTCCCTCGGAG 180
QY 13396 ctccctgtgcgtctcctgttcgcacccctccctcctaccgatacctgtccgccttct 13455
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QY 13456 cccctcgggaagcgtggcgctttctcctatagctcagcgtgtaggtatctcagttcgtgta 13515
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QY 13516 ggttcgttcgtcccaagctggcgctgtgtgcacgaaccccggttcacccgacgcgtgcgc 13575
D 301 GGTGCTTCGCTCCCAAGCTGGCGTGTGTGCACGAACCCCGGTTACGCCGACCGCTGCGC 360
QY 13576 cttatccgtaactatgctttagtcccaaccgggtaagacacagacttatcccccattgac 13635
D 361 CTTATCCGGTAACATATGCTTTGAGTCCAAACCCGGTAAGACAGGACTTATCCCACTGGC 420
QY 13636 agcagccactgggt-aacaggtatgacagcgaggtatgtagcggtgtacagagttct 13694
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QY 13755 tgaagccagttaccttcgcgaagaggttgtagctcttgcgcgaacaaacacacgcg 13814
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QY 13815 ctggttagcgggtggttt 13830
D 600 CTGGTAGCGGTGGTTT 615

RESULT 12
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LOCUS      Homo sapiens genomic DNA, 711 bp DNA GSS 14-APR-1999
DEFINITION Homo sapiens genomic DNA, 711 region, clone: PQ624A40, genomic survey sequence.
ACCESSION AG011497 AG004817
VERSION   AG011497.1 GI:3377385
KEYWORDS  GSS.
SOURCE    Homo sapiens DNA, clone:PQ624A40.
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
          Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 711)
AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE     Homo sapiens genomic DNA, chromosome 21q
JOURNAL   Published Only in Database (1998) In press
REFERENCE 2 (bases 1 to 711)
AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE     Direct Submission
JOURNAL   Submitted (02-AUG-1998) to the DBJ/EMBL/GenBank databases.
          Masahira Hattori, Kitasato University, Department of Science, JST
          Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan
          (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732,
          Fax:0427-78-9561)
          On Feb 5, 1999 this sequence version replaced gi:2828403.
COMMENT   AG004817: Submitted (03-Feb-1998).
FEATURES
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Best Local Similarity 94.0%; Pred. No. 4.2e-106;
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QY 14234 ttgttagtggaacaggttggtgatttgaacttttgcacaggaacggtctgcg 14293
D 78 TTGTTGTAGTGAGGACAGTGGTGTATTTGAACCTTTNGCTTTGCCACGAAACGGTCTCG 137
QY 14294 ttgtcgggaagatgcgtgatcgtgatccttcaactcagcaaaagttcgattattacaaca 14353
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QY 14354 agccgcgtcccgtaagtcagcgttaagtctgtccagtggttacaaccaattacaact 14413
D 198 AGCCGCGTCCCGTCAAGTCAGCGTAATGCTCTGCCAGTTTACACCAATTACCAATT 257
QY 14414 gtgattagaaacactcatcagcatcaaatgaaactgcaatttatttcattatcaggattat 14473

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Sun Feb 13 13:44:50 2000

minitransposon containing lacZ, URA3, and tet resistance.

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Db 258 CTGATTAGAAAACTATCGAGCATCAATGAACGCAATTTATTTCATATCAGGATTAT 317
QY 14474 caataccatattttgaaaaagccgtttctgttaataagaagagaaactcaccagcgagt 14533
Db 318 CAATACCATATTTTGAAGAGCGGTTCTCTGTAATGAAGAGAGAAACTCACCAGGCGGT 377
QY 14534 tccatagatggcaagatctgtatcgctgcgtatccgactcgcacatcaataac 14593
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Db 438 AACCTATTAATTTCCCTCGTCAAAAAATAAGGTTATCAAGTGAGAAATCACCAGTAGTGA 497
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Db 498 CGACTGAATCCGGTGAGAAATGGCAAGCNT--ATGCTTTCTTCCAGACTGTTTCAACAG 555
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RESULT 13
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DEFINITION V131H3 mrn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces
cerevisiae genomic 5', genomic survey sequence.
ACCESSION AQ875988
VERSION AQ875988.1 GI:6288232
KEYWORDS GSS.
SOURCE baker's yeast.
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycetales;
Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 794)
Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A.,
GesEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatidis, D., Jansen, R.,
Umansky, B., Heidtman, K., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R.,
Hager, K., Miller, P., Roeder, G.S., and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
Gene Disruption
Unpublished (1999)
Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumar@yale.edu
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Seq primer: GGCCTCTCTTCTTTGGAAGTAC
Class: transposon-tagged.
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without 2 micron or mitochondrial DNA was prepared in
pHS56-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mrn-3xHA/lacZ

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BASE COUNT 186 a 193 c 220 g 191 t 4 others
ORIGIN
Query Match 3.7%; Score 582; DB 88; Length 794;
Best Local Similarity 98.4%; Pred. No. 4.7e-105;
Matches 607; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
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Db 728 GCGCAACCCGACAGGGGCTATAAAGATANCCAGGGGTTTCCCCCTGNAAGCTCCCTCGT 669
QY 13405 ggcgtctctctgtccgacctgcggttacggatacctgcgccttttccctcttcggg 13464
Db 668 GCGCTCTCTGTTCCGACCCCTGCGGCTTCCGGAATACCTGTCGGCTTCTCCCTTCNGG 609
QY 13465 aagcgtgcgcttttctcatagctcacgctgtaggtatctcagttcgtgtaggtcggtcg 13524
Db 608 AAGCGTGGCGTTTCTCATATCAGCTCAGCGTGTAGGTATCTCAGTTTCGTGTAGGTGTCG 549
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QY 13645 tggtaacaggatttagcagacgaggtatgtaggcggtctacagagttcttgaagtggtg 13704
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RESULT 14
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DEFINITION DKFZp434H1527_sl_434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434H1527 3', mRNA sequence.
ACCESSION AL043613
VERSION AL043613.1 GI:5423000
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 579)
Bloecker, H., Boecker, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
EST (Bloecker, et al.)
Unpublished (1999)
On May 1, 1997 this sequence version replaced gi:2059366.

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DEFINITION	V31C11 mTn-3xHA/lacZ Insertion Library, strain Y2218 <i>Saccharomyces cerevisiae</i> genomic 5', genomic survey sequence.				
ACCESSION	AQ875935				
VERSION	AQ875935.1	GI:6288179			
KEYWORDS	GSS.				
SOURCE	baker's yeast.				
ORGANISM	<i>Saccharomyces cerevisiae</i>				
REFERENCE	Eukaryota; Fungi; Ascomycota; <i>Saccharomycetales</i> ;				
AUTHORS	1 (bases 1 to 795)				
	Ross-Macdonald, P., Roemer, T., Coelhof, P. S. R., Agarwal, S., Kumar, A.,				
	desEtages, S. A., Cheung, K. H., Sheehan, A., Symoniatas, D., Jansen, R.,				
	Umansky, L., Heidman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R.,				
	Hager, K., Miller, P., Roeder, G. S. and Snyder, M.				
TITLE	Large-Scale Analysis of the Yeast Genome by Transposon Tagging and				
	Gene Disruption				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Kumar A				
	Michael Snyder, Dept. of Mol. Cell. and Dev. Biology				
	Yale University				
	P.O. Box 208103, New Haven, CT 06520-8103, USA				
	Tel.: 203 432-0300				

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794	CGCGCTTCGTCAGCTTTATCTTAAGGCACGCGCCGCCCTACGAGGCATCAAAAATCAAC	735			
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734	GCTCAAGTCAAAGGTGCGGAATACCGACAGAGCTATAAAGATACACGAGCGTTTCCCGCT	675			
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674	GAAGCTCTTTCGTGCGCGCTCTCTCTTGACGCTGCCCTTACCGGATACCTGTCCGCC	615			
QY 13451	tttctcccttcgggaagcgtggcgctttctatagctacgctgtagtatctcagttcg	13510			
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614	TTTCTCCTTCGGAAAGCGGGCGCTTCATAGCTCAGCTGTAGTAGTATCTCAGTTCCG	555			
QY 13511	gtgtagctcgttgcctccaaagctggcgctgtgtgacgacaccccccttcagccgcgcgcg	13570			
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554	GTGTAGTGTCTTCGCTCCAAAGCTGGGCTGTGTGACGAACCCCGGTTACGCCGACCGC	495			
QY 13571	tgcgccttataccgggttaactactcgtcttgagttccaaaccggtaagaacagacttatcgca	13630			
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494	TGGGCGCTTATCCGGTAACTATACGCTTGAGTCCAAACCCGGTAAGACACGACTTATCGCA	435			

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us-09-190-246-1.rst

Sun Feb 13 13:44:50 2000

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Db 374 TTCTTGAAGTGGTGGCCTAACTACGCTACACTAGAGGACAGTATTGTGTATCTGGCT 315
OY 13751 ctgctgaagccagttaccttcggaagagttggtagctcttgaatcgcgcaaaacc 13810
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OY 13871 tctcaagaagatcctttgatctttctacgg 13901
Db 194 TCtCAAGAGATCCTTTGATCTTTTCTACTG 164

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Job time: 6472 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2000, 21:53:28 ; Search time 218.16 Seconds
(without alignments)
8526.984 Million cell updates/sec

Title: US-09-190-246-1

Perfect score: 15538

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Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 428588

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- 5: /cgn2_6/ptodata/2/ina/6_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2964	19.1	5682	3	US-08-663-998-4
6	2272.8	14.6	11663	2	US-08-446-932-1
7	2272.8	14.6	11663	2	US-08-801-263A-1
8	2272.8	14.6	11663	2	US-09-102-248-1
9	2271.2	14.6	11663	5	US-08-102-248-7
10	2271.2	14.6	11663	5	US-08-801-263A-7
11	2224.4	14.3	11717	5	US-09-102-248-4
12	2224.4	14.3	11703	5	US-08-801-263A-8
13	2222.8	14.3	11703	5	US-09-102-248-8
14	2222.8	14.3	11703	5	US-08-741-891-1
15	2311.6	14.2	16656	2	US-08-739-158-1
16	2211.6	14.2	16656	3	US-08-739-167-1
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22	1799	11.6	4296	6	PCT-US95-12642-15
23	1799	11.6	4352	6	PCT-US95-12642-16
24	1763	11.3	3993	1	US-08-316-950-14
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c 35 1762 11.3 6171 6 PCT-US95-12642-17
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c 39 1571.2 10.1 4928 1 US-08-345-913-1
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/07920281C
; Patent No. 5739026
; GENERAL INFORMATION:
; APPLICANT: Garoff, Henrik
; APPLICANT: Liljestrom, Peter
; TITLE OF INVENTION: DNA Expression Systems Based on
; TITLE OF INVENTION: Alphaviruses
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/920,281C
; FILING DATE: 13-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 828-103P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Semliki Forest Virus
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..11517
; OTHER INFORMATION: /label= genome
; OTHER INFORMATION: /note= "Semliki Forest Virus complete nucleotide
; OTHER INFORMATION: sequence, presented as a cloned DNA sequence; see
; OTHER INFORMATION: Figure 5."
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2728	ggtcacacaaatgaccatgcaaatgcagagcattttgcacctggctaccacaaattgat	2787			
182	GGTCAACCAATGACCATGCAATGCCAGACATTTTCCGACTGGCTACCAAAATTGAT	241			
2788	cgaagcagagactgacaaagacacactcatcttgatatcggaagtcgccttccaggag	2847			
242	CGAGCAGGAGACTGACAAAGACACACTCATCTTGATATGCGAGTGCCTTCCAGGAG	301			
2848	aatgatgtcttcgcacaaataaccactggtatgccctatcgacgcagcagaagaccccca	2907			
302	AATGATGTCTACGCACAAATACACTGCGTATGCCATATGCCAGCCTCCGGGAAGTGTGGATAGAGA	421			
2908	aaggtctgatagctacgacaaagaaactggcagcgccctccgggaagtgtgtagatagaga	2967			
362	AAGGCTGATAGCTACGCCAAGAAACTGCGACGCGCTCCGGGAAGTGTGGATAGAGA	421			
2968	gacgcagggaaaaatacacgcagactgcagacgtcatgctacgcacgcgtgaattccc	3027			
422	GATCGCAGGAAAAATACCGCACTCGCAGACCGCTCATGCTACGCCAGCGCTGAATCTCC	481			
3028	tacctttgctgcatacagactcacgtgtgctgacgcagcccggaagtggccgtatacca	3087			
482	TACCTTTGGCTGCATACAGACGCTACGCTGCTGATCGGCAGCGCAAGTGGCGGTATACCA	541			
3088	ggacgtgtatgctgtacatgcacaaacatcgctgtaccatcagcgcatgaagtgctcag	3147			
542	GGACGTGTATGCTGTACATGCACCAACATCGCTGTACCATCAGGCGATGAAGGTGTCAG	601			
3148	aacgcgctattgattgggtttgacaccaccgctttatgtttgacgcgctagcagcgc	3207			
602	AACGCGGTATGATTGGGTGTGACACCACCCCGTTTATGTTTGTGCGGCTAGCAGCGCG	661			
3208	gtatccaaacctacgcccaacactggcgacgagcaggtgttacaggccaggaacattagg	3267			
662	GTATCCAACTTACGCCCAAACTGGGCGCAGCAGCAGGTGTACAGCCGACGAACTAGG	721			
3268	actgtgtcagcactcttgcactgagggaaagactcggcaactgtccattctccgcaaga	3327			
722	ACTGTGTGCACATCTTGACTGAGGAGAGACTCGGCAAACTGTCCATTCTCCGCAAGAA	781			
3328	gcaattgaaaccttgcacacagctcatgtctcgttaggattctacattacacatgagag	3387			
782	GCAATGTAAACCTTCGCGACACAGTCATGTTCTCGGTAGGATCTACATTTGTACACTGAGN	841			
3388	cagaagctactgaggagctggcacttaccctccgtattccacctgaaagggtaaacaatc	3447			
842	CAGAAGCTTACTGAGGAGCTGGCACTTACCTCCGTATTCCACTGAAAGGTAAACAATC	901			
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•

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RESULT 2
US-08-663-9

b	3025	ACTCATAGCTCAGGAGGGTCCGCCCTTCATATCCACCGCTAAAGTACTGTGAGCGGTCT	3084
y	12968	ctccctccctcatcagcccaacaaacaaacttagcctccagagatgggaagaataaaa	13027
b	3085	CTCCCTCCCTCATAGCCCAACCACAACCTTAGCTCCAAGAGTGGGAAGAATTAAA	3144
y	13028	gcaagataggctattaagtgcagaggagagaaaaatgtccccaacatgtgaggaagtaat	13087
b	3145	GCAAGATAGGCTATTAAAGTGCAGAGGAGAGAAAAATGCCCTCCACATGTGAGGAAGTAAT	3204
y	13088	gagagaatcatagaatttctcgcttcctcgtcactgaactcgtcgtgcgtcggtcggtt	13147
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y	13148	cggctgcggagagcggtatcagetcaactcaaacgagcgttaatacggttatccacagaatca	13207
b	3265	CGGTCGGCGAGCGGTATCAGCTFCATCAAGGCGGTATACGGTTATCCACAGAATCA	3324
y	13208	gggataacgcaggaagaaacatgtgagcaaaagccagcaaaaggccaggaaccgttaa	13267
b	3325	GGGNATACGCAGGAAGAACATGTGAGCAAAAGGCCAGCAAAAGCCAGGAACCCGTAAA	3384
y	13268	aagtcgcgctgtgcgtgttccataggttcgcgcccccctgcagcagcatcacaaaaat	13327
b	3385	AAGGCGCGTGTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCCTGACGAGCATCACAAAAT	3444
y	13328	gaacctcaagtcagagtgggcaaacccgcagagactataaagataccaggcgcttccc	13387
b	3445	CGACGCTCNAGTCAGAGTGGCAAAACCCGACAGACTATAAAGATACAGCGCTTTCCC	3504
y	13388	cctggaagctccctcgtgcgtctcgtttccgaacctgcgccttacccgatacgtgcc	13447
b	3505	CCTGGAAGCTCCTCGTCGCGTCTCCTGTTCCGACCCCTGCCCTTACCGGATACCTGTGCC	3564
y	13448	gcctttcccttcoggaaagcgtggtcttctcatagctcaacgctgtaggttatcagtt	13507
b	3565	GCTTTTCTCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCACCGCTGATAGTATCTCAGT	3624
y	13508	tgggtgatggttcgttcgaagctgggctgtgtgcagaaacccccgttcagccgcac	13567
b	3625	TGCGTGTAGTCTGCTCGCTCCAAAGCTGGGCTGTGTGCAGCAACCCCGCTTCAGCCCGAC	3684
y	13568	cgtgcgcttaccggttaactatcgttgttgcacaacccggtaagacacagactatcg	13627
b	3685	CGCTGCGCTTATCCGGTAACFATCGTCTGAGTCCAACCCGGTAAGACACGACTTATCG	3744
y	13628	ccactggcagcagccactggtaacagvattagcagagcagvattagcaggtgtgtaca	13687
b	3745	CCACTGCGACGACCACTGGTAAACAGGATTAGCAGAGCGAGGATTGTAGCGGTGTCTACA	3804
y	13688	gagttctgaagtggtggcctaactacggtcatacactagaagaacagtatttggatatcgc	13747
b	3805	GAGTTCCTGAAGTGGTGGCCCTNACTACGGCTACACTAGAGAGGACAGTATTGGTATCTGC	3864
y	13748	gctcgtcgaagcaggttaocttcggaaaaagagtggttagctcttgatccggcaacaa	13807
b	3865	GCTCTGTGAAGCCAGTATACCTTCGAAAAAGAGTGTGGTAGCTCTTGTATCCGGCAACAA	3924
y	13808	accaccgtgtacgagtggtttttgtttgccaagcagcagattacgcgcagaaaaaaa	13867
b	3925	ACCACCGTGGTAGCGGTGTTTTTTTGTGTTGCAAGCAGCAGATTACCGCGCAGAAAAAAA	3984
y	13868	ggatctcaagaagatccctttgatcttcacgggggttcgagctcagtggaacgaacac	13927
b	3985	GGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGNAACGAAC	4044
y	13928	teacgttaaggaatttgatagattatcaaaaagatcttcacotagatcccttta	13987
b	4045	TCACGTTAAGGGATTTTGGTCATGAGATTATCAAAGSAITCTTCAOCTAGATCCTTTTA	4104
y	13988	aattaaaaatgaagttttaaatcaatctaaggtatataatgagtaaaacttgctgcaggt	14047

US-08-663-998-2

Query Match	19.1%;	Score 2967.2;	DB 3;	Length 5952;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 2983; Conservative	0;	Mismatches	8;	total

[illegible]

RESULT 3
 US-08-563-998-2
 ; Sequence 2, Application US/08663998
 ; Patent No. 5846945
 ; GENERAL INFORMATION:
 ; APPLICANT: HUEBNER, Robert C.
 ; APPLICANT: NORMAN, Jon A.
 ; APPLICANT: LIANG, Xiaowu
 ; APPLICANT: CARNER, Kristin R.
 ; APPLICANT: BARBOUR, Alan G.
 ; APPLICANT: LUKE, Catherine J.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: ADMINISTERING BORRELIA DNA
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Curtis, Morris & Safford, P.C.
 ; STREET: 530 Fifth Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/663,998
 ; FILING DATE: 06-JUN-1996
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kowalski, Thomas J.
 ; REGISTRATION NUMBER: 32,147
 ; REFERENCE/DOCKET NUMBER: 454312-2440
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-840-3333
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5952 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)

RESULT 4
US-08-663-998-3
Sequence 3, Application US/08663998
Patent No. 5846946
GENERAL INFORMATION:
APPLICANT: HUEBNER, Robert C.
APPLICANT: NORMAN, Jon A.
APPLICANT: LIANG, Xiaowu
APPLICANT: CARNER, Kristin R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: LUKE, Catherine J.

RESULT

RESULT 4
TSC-08-663-998-3

US-08-663-998-3 Application US/08663998
sequence 3

; Sequence 3, Application 3, 5846946

Patent No. 5846946

GENERAL INFORMATION:

APPLICANT: HUEBNER, Robert

APPLICANT: NORMAN, JON A.

APPLICANT: LIANG, Xiaowu

APPLICANT: CARNER, Kristin R.

APPLICANT: BARBOUR, Alan G.

APPLICANT: BARBOUR, Alan G.
APPLICANT: LUKE, Catherine J.

;; APPLICANT: LUKE, CATHLEINE S.

Query Match	19.1%	Score 2964	DB 3	Length 5676	
Best Local Similarity	99.6%	Pred. No. 0			
Matches 2981	Conservative	0	Mismatches	10	Indels 1; Gaps 1;
12548	gatcagatctgctgctcctcttagttgcagccatctgtttgtttgccccctccccctgc	12607			
2441	GATCCAGATCTGTGTGCCCTTCCTAGTTGGCAGCATCTGTTCTTTGCCCCCTCCCCGTGC	2500			
12608	cttctctgacccctgggaaggtgcacactccacactgctcttctctaaataaatgagaaattg	12667			
2501	CTTCTCTGACCCCTGGAAGGTGCCACATCCCACATGCTCTTCTTAAATAATGAGAAATTG	2560			
12668	catgcgattctcgaatgagtctattctattctctgggggtgggggtggggcagacagca	12727			
2561	CATCGCATTTCTTCAGTAGTGTCTATTCTTATTCTGGGGGTGGGTGGGGCAGCACAGCA	2620			
12728	agggggagagattgggaagacaatagcaggcatgctggggatgcagttgggtctctatgggta	12787			
2621	AGGGGAGGATTGGGAAGACAATAGCAGCATGCTGGGGATCCGGTGGGTCTATGGGA	2680			
12788	ccaggtgctgaagaattgacccgttctctctctggggccagaagaagcagcgacatcccc	12847			
2681	CCCAGTGTGTGAAGATTGACCCGGTTTCTCTGGGGCCAGAAAGCAGCGCACATCCCC	2740			
12848	tctctgtgacacacccctgtccagccctggttcttagttccagcccccactataggac	12907			
2741	TTCTCTGTGACACACCCTGTCCAGCCCTGGTTCTTAGTTCAGCCCCACTCATAGGAC	2800			
12908	actcatagctcagggaggtccgctctcaatccaccgcgttaagtacttgagcggtct	12967			
2801	ACTCATAGTCTAGGAGGCTCGGCTTCAATCCACCCGCTAAAGTACTTGGAGCGGTCT	2860			
12968	ctccctccctcatcagcccccacaaacctagctccccaagatggggaacaaattaaa	13027			
2861	CTCCCTCCCTCATCAGCCCCACAAACCAACCTAGCCTCCAGCTGGGAAGAAATTAAA	2920			
13028	gcagatgagggtattaagtcagaggagagaaaaatgctcccaactgtgaggaagtaat	13087			

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[illegible]

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5
RESULT
US-08-63998-4
; Sequence 4, Application US/08663998
; Patent No. 5846946
; GENERAL INFORMATION:
; APPLICANT: HUEBNER, Robert C.
; APPLICANT: NORMAN, Jon A.
; APPLICANT: LIANG, Xiaowu
; APPLICANT: CARNER, Kristin R.
; APPLICANT: BARBOUR, Alan G.
; APPLICANT: LUKE, Catherine J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; ADMINISTERING BORRELIA DNA
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,998
; FILING DATE: 06-JUN-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalski, Thomas J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454312-2440
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-840-3333
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5682 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-663-998-4

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Query Match          19.1%; Score 2964; DB 3: Length 5682;
Best Local Similarity 99.6%; Pred No. 0;
Matches 2981; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
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QY	14287	gtctcggttctgggaagatcggtgatctcatctcaactcagcaaaagtctcgattat	14346
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QY	14347	tcacaagccgctccgctcaagtcagcgtgaatgctctgccagtggtacaacaatta	14406
Db	4241	tcacaagccgctccgctcaagtcagcgtgaatgctctgccagtggtacaacaatta	4300
QY	14407	accaatttgattagaaaaactcatcgagatcaaatgaaactgcaatttattcatatca	14466
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QY	14467	ggattatcaatccatttttgaaaaagcggtttcttgaatgaaggagaaaaactcaocg	14526
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QY	14527	aggcagttccataggatggcaagatcctggtatcggtctcgatcccgactcgccaaca	14586
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QY	14647	tgagtgcagctgaatccggtgagaatggcaaaagcttagctattcttccagacttgt	14706
Db	4541	tgagtgcagctgaatccggtgagaatggcaaaagcttagctattcttccagacttgt	4600
QY	14707	tcacagccagcattacgtctgcatcaaaactcgtcgatcaccaaaaaacggttattc	14766
Db	4601	tcacagccagcattacgtctgcatcaaaactcgtcgatcaccaaaaaacggttattc	4660
QY	14767	attcgtgattgcctgagcagagacgaatacgcgactcgctgttaaaagacaattacaa	14826
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QY	15007	gtcagccagtttagtctgaccatctcatctgttaacatcattggcaacgctaccttgcca	15066
Db	4901	gtcagccagtttagtctgaccatctcatctgttaacatcattggcaacgctaccttgcca	4960
QY	15067	tgtttcagaaaacactctggcgatcgggtctcccatcaaatcgatagattgtgcacact	15126
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QY	15187	tttaatcgcgccctcgagcaagacggtttccgcttggaatgagctcataacgcttctctgta	15246
Db	5081	tttaatcgcgccctcgagcaagacggtttccgcttggaatgagctcataacgcttctctgta	5140

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Sun Feb 13 13:44:47 2000

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,932
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
US-08-446-932-1

Query Match 14.6%; Score 2272.8; DB 1; Length 11663;
Best Local Similarity 58.4%; Pred. No. 0; Mismatches 2892; Indels 237; Gaps 14;
Matches 4385; Conservative

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QY 14767 attcgtgattgcgcctgagcgagacgaatacgcgctgctgttaaaagacaaattacaa 14826
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Db 4667 ATTCTGATTGCGCTGAGCGAGACGAATAACGCGATCGCTGTAAAGACAAATTACAA 4726
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QY 14827 acaggaatcgaatcaaacgcgcgagaaacactccgcgcgcgcatacaacaattttcacct 14886
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Db 4727 ACAGGAATCGAATCAACCGCGCAGAGAACACTGCCAGCGCATCAACAATATTTTCACT 4786
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QY 14887 gaatcaggatatcttctaatacctcgggaatgctgttttcccggggatcgcagtggtgagt 14946
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Db 4787 GAATCAGGATATCTTAATACCTTGGAAATGCTGTTTCCCGGGGATCGCAGTGTGAGT 4846
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QY 14947 aacctatcatatcaggagtaacgaataaattgcttgatggtcggaaaggaggaataattcc 15006
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Db 4847 AACCATGTCATATCAGGAGTAGCGATAAATGCTGTGTTGCGGAAGGCGATAAATTC 4906
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QY 15007 gtacgcaggttagtctgaccatctcatctgttaacatcattggcaacgtcactttccca 15066
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Db 4907 CTAGCAGCTTAGTCTGACCATCTCATCTGAACATCATTTGGCAACGCTACCTTTTGCA 4966
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QY 15067 tgttcagaaacaaactctcgtcgcacatcgttcctccatacaatcgatagattgctgcacct 15126
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QY 15127 gattgcccgcattattgcgagccattttatacccatataataatcagcatccatgttgaa 15186
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QY 15187 tttaatcgccgcctcgcgagaaagcgttccggttgatggtcgcataacgcttccttgta 15246
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QY 15247 ttactgtttatgaagcagacagttttattgttcctatgatgatattttattttatgca 15306
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QY 15307 atgtaacatcagagattttgagacacaaactggtcttcccccccccccccattatgaagc 15366
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QY 15367 atttaccaggtttatgtctcatgagcggtatcacattattgaatgtatttagaaataaa 15426
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Db 5327 CAATAGGGGTTCCGCGCACATTTCCCGAAAGTGCCACCTGACGCTTAAGAAACCAAT 5386
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QY 15487 attatcatgacattacattataaaataggcggtatcacagggccctttcgtc 15538
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Db 5387 ATTATCATGACATTAACTATAAATAAGCGGTATACAGAGGCGCTTTCGTC 5438
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RESULT 6
US-08-446-932-1
Sequence 1, Application US/08446932
Patent No. 5639650
GENERAL INFORMATION:
APPLICANT: Johnston, Robert E.
APPLICANT: Simpson, Dennis
APPLICANT: Davis, Nancy L.
TITLE OF INVENTION: CDNA Clone for South African
TITLE OF INVENTION: Arbovirus No. 5639650 86
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: NC
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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731	AAATGTTCTGATAATCAGGAAGAGGAGTTGAAGCCCGGGTCACGGGTTATTTCTCCGT	790
3364	agatctacattgtacactgtagacagaagctactgagagctgtggcacttaccctcgt	3423
791	TGGATCGACACTTTACCCAGAACACAGACGCCAGCTTTCGAGAGTGGCATCTTCCATCGGT	850
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851	GTTCACACTTGAAGGAAAGCAGTCTGACACTTCCGCTGTGATACAGTGTGAGCTGCCA	910
3484	agggtacgtagttaagaaatcactatgtgccccggcctgtacgtgtaaacggtagggtga	3543
911	AGGCTACGTAGTGTGAAGAAATCCACATCATGTCCTCCGGATACGGGAGAACCGTGGGATA	970
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3724	tcagagtagtgtgtgaagggaagacacagcgaacactaaacacgatgaagaactatct	3783
1151	CACGGAACTCGTCAATTAACGGTAAGACTAACAGGAACACCAATACCATCAAAATTA	1210
3784	gtctccgattgtggcgtgcgcttagcaagtggcgagggaatacaaggcagacctga	3843
1211	TCTGCCAATCATTTGCACAAGGTTTCAGCAATATGGCCCAAGGCGCAAGAAGATCTTGA	1270
3844	tgatgaaaacctctgggtgtccgagagaggtctacttctgtctgtctgtgtggcatt	3903
1271	CAATGAAAAAATGCTTGGCCACCAGAGAGCGCAAGCTTACATATGCTGCTGTGGGGCTT	1330
3904	taaaacgaggaagatgacacacatgtacaagaacacagacacccacagacaatagtgaagg	3963
1331	TCGCACATAAGAAGTGCACTGTTCTATCGCCACCTTGAACGCGAGACATCGTAAAGT	1390
3964	gccttcagagtttaactgtctgtctccgagacctatggtctacagcctcgcaatccc	4023
1391	CCAGGCTCTTTTACGGCTTTCCCCATGTATCCGTATCGCACTACTCTTTGCCCATGTC	1450
4024	agtcagatacagcattaagatgcttttggccaaagaagaccaaagcgagagtttaatacctgt	4083
1451	GCTGAGGCGAGAAGATGAATTTGGCATTTACAAACAAAGAGGAGGAAAACTGCTGCAAGT	1510
4084	tctcgagcgt-----cgtcagccaggatgctgtgaacaagagagagagagaggttga	4137
1511	CCCGAGGAATTTAGTTATTTAGGAGGCCAAGCTGTTTCGAGGATGCTCAGGAGGAATCCAG	1570
4138	ggccgaggtgtactagaagaccttaccacctctgtccc-----catcgccgcggcgagac	4194
1571	AGCGAGAGAAGTCCCGAGAACACTCCACCATTATGTGTCAGACAAAGGTATCGAGCAGC	1630
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1631	TCCGGAAGTTGTCTGCCAAGTGGAGGGGCTCCAGCGGACACCGAGACGACTCGTCTGA	1690
4255	aacaccttcagcgctgtgaagatcacgcgcacagccgcaacgactactactaggaaatta	4314
1691	AACCCCGCGGGTCATGTAAAGATTAATACCTCAAGCAAAATGACCGGTATGATCGGACAGTA	1750
4315	cgtagttctgtcccccgacacctgtctcaagagctccaagttggcccccggtgcacctct	4374
1751	TATCGTTGTCTCGCCGATCTCTGTCTGAAGACGCTTAACCTCGCACAGCACACCCGCT	1810

Qy	4375	agcagagcaggtgaaaaataataacacataaagcgaggccgggttaccaggtcgacgg	4434
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Qy	4435	atacgagcgaagggtctactacacatgtggatcgggccattccggtccctgaggtttcaag	4494
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Qy	4495	tttgagcgagcgcccaactatggtgtacaacgaagaggagttcgtcaacagagaactata	4554
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Qy	4555	ccattatggccgtttcacgagaccctcgctgaacaccgcagcagggagaactacgagaaagtcag	4614
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Db	2051	GGCAGAGCTCGCAGAAACAGAGTACGTTTTCGCTGCACAAGAAGCGATCGCTTAAGAA	2110
Qy	4675	aaaggaagcgttcgggtttggtgttggtggagagctaaaccaaccccccggttcccatgaatt	4734
Db	2111	GGNAAGAAGCCTCAGGACATGTGCTTTCGGGAGAAGTGAACCAACCCGCGCTATCAGGA	2170
Qy	4735	cgctacgaagggtgaaagatcagcgccctcgccaccataataagactacagtagtaggagt	4794
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Qy	4795	ctttggggttcgggatacaggcaagttgtctattattaagagcctcgtagccaaacacga	4854
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Qy	4855	tctgttcaccagcggaaggaaggaactccaggaataatgttaacagacgtgaagaagca	4914
Db	2291	TCTTGTACCAGCGGAAGAAAGAAACTCCGCGAAATTTGAGCCCGACGTGTACGGCT	2350
Qy	4915	cgcgggaaggggacagtgagggaacagtgactccctctctctctctctctctctctctctc	4974
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Qy	5035	octaattgctctgtttaaactcctcggagcaagtggtgttatcgggagaccccaagcaatg	5094
Db	2471	CTTGATTTGCAATCGTCAGACCCCGTAAGAAGGTAGTACTATCGGAGACCCCTAAGCAATG	2530
Qy	5095	cggattctcaatgatgatcagcttaagtgaaacttcaaccac-----aacatctg	5145
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Qy	5146	cactgaagtatgtcataaagtatatccagacgcttgacggtccagtcacggccatcgt	5205
Db	2591	TACCAAGACATTTCTACAAGTTTATCTCCGAGCTTGACACAGCCAGTCACGGCTATTGT	2650
Qy	5206	gtctacgttgactacggaggaagatcgcaacgcaaccccgctgcaacaaaccataat	5265
Db	2651	ATCGACACTGCATTACGATGGAAAAATGAACACCAACAAACCCGTGAAGAAGAACATCGA	2710
Qy	5266	catagacacacagacagacccaagcccaagccagggagacatcgtgttaacatgcttcg	5325
Db	2711	AATCGACATTCACAGGGGCCAAGCCCAAGCCAGCGGGGACATCATCTGACATGTTTCCG	2770
Qy	5326	aggtcgggcaagagcgtcagttggactacccgttgacacgaagtcatgacagcagc	5385
Db	2771	CGGGTGGGTTAAGCAACTGCAAAATCGACTATCCCGGACATGAGGTAATGACAGCGCGGC	2830
Qy	5386	atctcagggcttcaccgcaaggggtatccgctgaagcgagaaggtgaatgaataatcc	5445
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Qy	5446	cttgtatccccctcgtcggagcagtgaaatgtactgtcagcgcactcagagataggct	5505

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QY 7639 gtcgttac---gaggggttgacttgagactggaccacagactcgtcttccactgcccagcga 7695
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QY 7714 ttgagtcgtgtgacatcgactcgtactcagcagcgaatggtcccatagtgtagcggc 7773
Db 5225 ACTCTTTTCGAGCTTTAGCGGATCGGACACTACCGAAGCGAGGTGGTGGCTGACGT 5284
QY 7774 tgagctacacctgaaccccgagcgcgcgagactcgcggacctggcgagagtgtcacccctgaacc 7833
Db 5285 CCATGCCGTCCAGAGAGCTCCCTGCTTCACCGCCCAAGGCTAAAGAAATGCCCGGCT 5344
QY 7834 cgcagacatgtggacctcgagaccgcgacttcctcacgcgcgcgcgaagagc----- 7888
Db 5345 GCGAGCGGCAAGAAATGCAGGAGAGCAACTCCACCGCAAGCACCAAGCTCTGCGGACGA 5404
QY 7888 -----tgacataccttgctcccgcgcgcgagcagcagcgt 7923
Db 5405 GTCCCTTCACCTTTCCTTGTATGGGTATCTATATCTTCGGATCCCTTTTCGACGGAGA 5464
QY 7924 gcggcgccgagaaagccgacgacctgcgccaagagactcgttttaggaacaagctgccttt 7983
Db 5465 GATGGCCCGCTTGGCAGCGGCAACACCCCGGCAAGTACATGCCCTACGGATGTGCCCTAT 5524
QY 7984 gacgttcggcgacttgacgacgacgagtgatcgatcggttggcctcccggaattacttcgg 8043
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QY 8044 agacttcgac----- 8054
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Db	7322	GGGTAAACCGGTCCACGCCGACGATGAGCAAGACGAGACAGAAGACGCGCTCTGCTAGA	7381
Qy	9739	cgagggttagcaagtggttccgcgacaggcgttggggggccgaactggaaggtgagcactaacatc	9798
Db	7382	TGAACAAAGCGGTGGTTTAGGTAGGTATTAACAGACACCTTAGCATTGGCCGTGGCAC	7441
Qy	9799	taggtatgaggtagaaggctgcataaagtatcctcatgccatggcaccttggcgcaggga	9858
Db	7442	TGGGTATGAGGTAGAACACATCACACCTTGCTCTGCTGGCATTGAGAACATTTGCCCCAGAG	7501
Qy	9859	caattaagcggtttaagaaattgaggagacctgttatcacctctaogcggctcctagatt	9918
Db	7502	CAAAAGACGATTCAGCCATCAGAGGGGAAATAAAGACATCTTACGGTGGTCTAAATA	7561
Qy	9919	ggtgcggttaataca	9932
Db	7562	GTCAAGCATAGTACA	7575

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Query Match	14.6%	Score 2272.8	DB 2	Length 11663
Best Local Similarity	58.4%	Ident. No. 0		
Matches 4385	Conservative	Mismatches 2892	Indels 237	Gaps 14
2644	agtcattgtgattgaggtcagacgcccattcaacgaattttgacgaaggaattccc	2703		
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74	AGTTAACGTAGACGTAGACCTCAGAGTCGGTTGTCGTCAACTGCAAAAGAGCTGCC	133		
Qy				
2704	gtcgtttagagtgagtcattgaggtcaacacaaatgacctgcaaatgccagagcatt	2763		
Qy				
134	GCAATTTGAGGTAGTACACAGCAGGTCCTCCATAGTACCATGCTAATGCCAGAGCAT	193		
Db				
2764	ttcgcaactggctaccaaattgatcgcagcaggagactgacaaagacacactcatcttga	2823		
Qy				
194	FTCCGATCTGGCCAGTAATACTGAGCTGGAGGTTCTTACACACGACGAGTATTGGA	253		
Db				
2824	tatcggaagtgcgcttcagagaatgatgtctacgcaacaaatacactggatgcgcc	2883		
Qy				
254	CATAGCGAGCGACCGGCTCGTGAATGTTTCCGACACCATACCTATGCTGGCC	313		
Db				
2884	tatgcagcagcagacagcccccgaaggtctogatagtctagcgaagaaactgcagcggc	2943		
Qy				
314	CATCGGTAGTCAGAAGACCCGGACCGCATGATGAATATGCCAGCAATGCCGGA	373		
Db				
2944	ctccgggaagtgtcgtatagagagatcgaggaataatcaccgacctgcagaccgtcat	3003		
Qy				
374	AGCATGTAGATTACAAACAGAACTTCGATGAGAGATCAAGGACCTCCGGACCTG	433		
Db				
3004	ggctacgcagcagcgtgaattctctacatttgcctgcatacagacactcagtgctgatc	3063		
Qy				
434	TGATACACCGGATGCTGAAACGCCATCACTTGCCTTCACAAACGATGTTACCTGCA	493		
Db				
3064	ggcagcgaagtggccgtatcacaggagcgtgatcgtgtacatgcacaaacatcgcgtga	3123		
Qy				
494	CGGTGCCGAGTACTCCGTCATCGAGGACGTGTA---CATCAACGCTCCCGGAATATTTA	550		
Db				
3124	ccatcagcagcagatgaagggtgcagaacgcgtattggattgggtttgacacacccggt	3183		
Qy				
551	CCACGAGCCTATGAAAGGCGTGCGGACCCCTGACTGTGATGTGCTTCGCACACCCAGTT	610		
Db				
3184	tatgttgacgcgtagcagcgcgtatccaaactlaccgcacaaactggcgacagca	3243		
Qy				
611	CATGTTCTCGGCTATGCGAGTTCGTACCTGCAUACAAACACAACTGGCGGACGAAAA	670		
Db				
3244	gggtgtacagccaggaacataggaactggtgcagcatccttgactgaggggaagactcgg	3303		
Qy				
671	AGTCCTTGAGCGCGGTAAACATCGCACTCTGCACCAAAAGCTGAGTGAAGCGAGACAGG	730		
Db				
3304	caaacgttccattctccgcaagaagcaattgaaccttgcacacagtcattctcgt	3363		
Qy				
731	AAAGTTGTGATGTAATGAGGAAGAGGAGTTGAAGCCCGGCTCACGGGTTTATTTCTCCGT	790		
Db				
3364	aggtatcatattgtacactgagacagaaagctactgagagctggcacttaccctccgt	3423		
Qy				
791	TGGATCGACATTTACCCAGAACACAGCCAGCTTGCAGAGCTGGCATCTTCCATCGGT	850		
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3424	attccacctgaaggtaaacatctttaactgtaggtggatataccatcgtcatcgtga	3483		
Qy				
851	GTTCACITGAAAGGAAAGCAGTGTGATCTTGCCGCTGTGATACAGTGGTGAAGTGC	910		
Db				
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Qy				
911	AGGCTACGTAGTGAGAGAAATCACCTACGTTCCCGGGATCACGGGAGAAAACCGTGGG	970		
Db				
3544	cgcgctgacgtatcacgcggaggggattccttagtgtgaagacacacactcgaag	3603		
Qy				
971	CGCGGTTACAAATAGCGAGGGGCTTCTGCTATGCAAGATTACCGATACAGTAAAGG	1030		
Db				
3604	agaaagtgctcattccctgtatgcacctaagctccctcaaccatctgtatcaaatgac	3663		
Qy				
1031	AGAACGGGTATGCTCCCGTGTGACGATATATCCCGGCCACCATATGCGATCAGATGAC	1090		
Db				

Qy	3664	tggcatactagcgaccgacgctcacaccgaggagcgacagaagtcttagtgggttgaa	3723
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Qy	3724	tcagagatagttgtgaacggaagaacacagcagcaaacctaaacgatatgaagaactatct	3783
Db	1151	CCACCGAATCGTCATTAAACGGTAAGACTTAACAGGAACCAATACCATCCATCAAAATTACCT	1210
Qy	3784	gcttcogattgtggcgtgcatttagcaagtggcgaggggaatacacaagcgacacttga	3843
Db	1211	TCGTCCAATCATTGCACAAGGTTTACAGAAATGGGCCAAGGAGCGCAAGAAGATCTTTGA	1270
Qy	3844	tgatgaaaacctctgggtgtccgagagaggttcaattacttctgctgctgtgtgggcatt	3903
Db	1271	CATGTAAAAAATGCTGGGCACAGAGAGCGCAAGCTTACATATGCTGCTTGTGGCGCTT	1330
Qy	3904	taaaagaggaagatgcacaccatgtacaagaacacagacacccagacaaatagtgaaggt	3963
Db	1331	TCGCACATAAGAAAGTGCACCTCGTTCTATCGCCACCTTGAAACGCGAGACCATCGCTAAAGT	1390
Qy	3964	gcttcagaggtttaatcgttgcgtcatcccagagcctatggtctacaggccctcgcaatccc	4023
Db	1391	CCGAGCCTCTTTTAGCGCTTTCCCATGTCTATCCGTATGGACTACCTCTTGGCCATGTC	1450
Qy	4024	agtcagatcacgcattaaagtcttttggccaaagaagacacagcgaggttaatacactgt	4083
Db	1451	GCTGAGGCAAGATGAATTTGGCATTACACCAAGAAAGAGGAGAAACTGCTGCAAGT	1510
Qy	4084	tctcgacgcgt-----cgtcagccagggatgctgaaacaagagagagagaggttgga	4137
Db	1511	CCCGAGAGAAATAGTTATGGAGGCCAAGGCTGCTTTCGAGGATGCTCAGGAGGAATCCAG	1570
Qy	4138	ggcagcgtcactagagaagccttaccacccctcgtccc---catcgccgcgcggagac	4194
Db	1571	AGCGAGAAAGTCCGAGAAGCACTCCCACTATTAGTGGCAGACAAAGGTATCGAGGACG	1630
Qy	4195	gggagtcgtcgacgtcgacgttgaagaactagagtatcacgcaggtgcaggggtcgttga	4254
Db	1631	TGCGGAAGTTGCTTCGCGAAGTGGAGGGGCTCCAGGGGGACACCGGAGCAGCACTCGTCGA	1690
Qy	4255	aacacctcgacgcgcttgaagtcaccgcacagcgcaacgacgactactactaggaatata	4314
Db	1691	AACCCCGCGGGTCATGTAAGGATATTAACCTCAAGCAATATGACCGTATGATCGGACAGTA	1750
Qy	4315	cgtagctctgtcccgacagaccgtctcaagagctccaagttggcccccgtgcacccctc	4374
Db	1751	TATCGTGTCTCCCGGATCTGTGTGAAGAACGCTAAACTCGCACGACACACCCCGT	1810
Qy	4375	agcagcgaggtgaaataataacacataaacgggagggcgcggttaccaggttcgacgg	4434
Db	1811	AGCAGACCAGTTTAAGATCATACGCATCCCGNAAGATCAGGAAGGTATGCAAGTCCGAACC	1870
Qy	4435	atatcgccaggggtcctactaccaatgtggaatcgggccattccggtccctcgatttcaagc	4494
Db	1871	ATACGACGCTTAAGTACTGATGCCAGAGAAAGTGCCTGTCACATGCCCCAGATTCATTAGC	1930
Qy	4495	tttgagcgagcgccactatggtgtacaacgaaggaggttcgtcaacaggaaactata	4554
Db	1931	ACTGAGTGAGCGCCACGCTTGCTGTACACGAAGAGGTTGTGAACCCGACAGCTGA	1990
Qy	4555	ccatattccgttcaaggacgcgtgcgtgaacccgacgagagaaactacagaaagtcag	4614
Db	1991	CCATATGCCATGTCACGCTCCGCTTAAGAAATACAGAGGAGCAGTACAAAGTTACAAA	2050
Qy	4615	agctgaagaactcagcgagatcgtgttcagcgtagataaaaaatgctgcgtcaagag	4674
Db	2051	GGCAGAGCTCGAGAAACAGAGTACGTGTTTGAGCTGGACAAGAAAGCAATGCGCTTAGAA	2110
Qy	4675	agaggaagcgtcgggtttgggtgttggggagagactaaccaaccccccgcttcactgaatt	4734
Db	2111	GGAAAGACCTTCAGACATTGCTCTTTGGGAGAACTGACCAACCGCCCTATCACCAACT	2170
Qy	4735	cgcttcagaagggctgaagatacaggccgtcgccaccataaagactacagtagtaggagt	4794

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Db 2171 AGCTCTTGAGGACTGTAAGACTTCGACCCGCGTCCGTAACAGGTGTAACAATAGGAGT 2230

QY 4795 ctttggtgtccgggatacagcaagtctgtctattattaagagcctcgtgaccaaacacga 4854

Db 2231 GATAGGCACACGAGATCGGGCAAGTCAGCTATCATCAAGTCACTGTTCAGCGACGTGA 2290

QY 4855 tctgtccacagcgcgaagaagagagaactgccaggaaatagttaacgacgtgaagaagca 4914

Db 2291 TCTGTTTACACGCGGAAGAAAGAAATGCCGGAATTTGAGCCGACGTGCTACGGCT 2350

QY 4915 ccgggggaaggggacaagttagggaaacagtgactcccatctgtaaacagggtgtcgtcg 4974

Db 2351 GAGGGGATCGAGATCAGCTCGAAGACAGTGGAATTCGGTTATGCTCAACGGATGCCACAA 2410

QY 4975 tgcgtgagacatcctatatgtgagcagagcttgcgttgccattcccggtactctgtgpc 5034

Db 2411 AGCGTGTGAAGTGTCTGTATGTTGAGAAAGCGTTCGGTGGCCACGAGGACACTACTTGC 2470

QY 5035 cctaattgctctgttaaacctcggagcaaatggtttatgcgagagcccccaagaatg 5094

Db 2471 CTTGATTGCAATCGTCAGACCCCGTAGAAGGTAGTACTATGCGGAGACCTTAAGCAATG 2530

QY 5095 cggattctcaatatgatcagcttaagtgaactcaaccac-----aacatctg 5145

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QY 5146 cactgaagtatgtcataaagtatatccagactgtgcaagcgttcgaagtcgcgggcacgtg 5205

Db 2591 TACCAAGACATTCACAGTTTATCTCCCGACGTTGCACAGCGAGTCACGGCTATTGT 2650

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QY 5326 aggtggaagcagctgcagttggaactacggtgacagcaagtcacgacagcagcagc 5385

Db 2771 CGGGTGGGTTAAGCAACTGCAATTCGACTATCCCGGACATGAGGTATATGACGCGCGGC 2830

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QY 5446 ctgtgatccctcgtctggagcagtcgaatgactctgctgcgcgcactgagataggt 5505

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Db 3071 AACAGTCCCGCTCCCGGTACCAATTCGTTTCAGTGCAGACATAAGTTCGTGGCGGAA 3130

QY 5686 aagcctgtgtcctgtcctgacactgcggaatacagattgaacagcagaggtgagc 5745

Db 3131 AGCACTGGAACCGATACTGGCCACGCGCGGTATCGTACTTACCGGTGCGCAGGAGCA 3190

QY 5746 cataattacagcatttaaggagagacagcttactctccagttggtgacctgaatgaat 5805

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QY 5806 ttgcaccaagtactaggttgacctggacgtgacctgttcttctgccccgaaggtgct 5865

3251	TTGCATTAAGTTTTTCGGCATGTGACATTGCACAAGCGGGCTGTTTTTCCAAAACAGACGATCC	3310
5866	ccgtgtattaccagaaac-----cactgggataacagacctgg	5904
3311	GTTAACGTTACCATCTCGCGACTCAGCGAGCGCCAGTAGCTCAATTGGGACAAACAGCCGAG	3370
5905	tgaagagatgatgatgaatcgcgcgaacagctgcgcaggtcggaagctagacataacctt	5964
3371	AACACGCAAGTAATGGGTACGATACGCCGTTTCGCGCGAACTCTCCCGTAGATTCCGGT	3430
5965	cttgaagggcagtggtgcatacgggcaagcagcgagcttatcgcagaagaataatccaacc	6024
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6025	gctttctgtcgtggacaatgtaattcctatcaacgcgaggtgcgcgcacgcctgttggc	6084
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6085	tgagtacaagacggttaaaaggcagtaggttgagtggctggtgctcaataaagaagaagggtta	6144
3548	CGAGCACAAAGGAGAAACACCGCGCGCTCGAAATAATCTTTGAGCCAGTTCAACACACCA	3607
6145	ccacgtcctctgtgtagtgagtgacaacctgcttgcctgcacgcagggctcaacttggtt	6204
3608	CTCGTACTTGTGATCTCAGAGAAAAAATTGAAGCTCCCCACAAGAAATCGAATGGAT	3667
6205	gtcacccgtgaattgcacagggcgcagtaggtgtctacgacctaaagttagaactccgcgc	6264
3668	CGCCCCGATTGGCATATACCGCGCGCAGATAAGAACTACAACCTGGCTTCGCGTTTCCGCC	3727
6265	tgacgcgcgcaggttcacactgctcttctgtaacattccacggaattcagaaatcaaca	6324
3728	GCAGGC---ACGGTACCACCTGGTTTCATCATATTGGAACATAATACAGAAACCATCA	3784
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6385	actgtataaacccgcgcgc---ctctgatgagagcttaccgatacgcgcgataaaatcag	6441
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6442	cgaagccgtgtttctcctcttaacgcgaaagtctctgtctgcaagagtggtgcgccgga	6501
3905	TGAGGAGGTAGTACCGCTCTTGCCAGAAAAATTTGTACAGAGTGCTGCACGAGGCCGAGA	3964
6502	tgtgtcacacgaataacagaagtgcttctgtctctccaaacttgacaacgcgaagaag	6561
3965	GTGCGTCTCAAGCAATACAGAAATGACTGATTTTCGCACAACTAGACAAACGCCGCAC	4024
6562	accctctacgtcacacagatgaataaccaagctgagtgccgtgtatgccggagaagccat	6621
4025	ACGACAATTACCCCGCCATCAATTGAATGTGTGATTTTCGTCGCGTGTACGAGGTTACAG	4084
6622	gcacacgcgcgggtgtgcaccatctcacaggttaagagagcagacatagccagtgccac	6681
4085	AGACGGAGTTGGAGCGCGACCGCTGTACCGCTACTTAAGGGAGAACATTGCTGATTGTCA	4144
6682	agaagcgctgtggtttaacgcagcagctaaccccgctggaactgtaggggagtcgctatgcag	6741
4145	AGAGGAAGCAGTTGTCAATGCAGSCCAATCCACTGGGACACAGGAGAGTCTGCGC	4204
6742	ggccgtggcgaaagaaatggccgtcagcccttaaggagagcagaacacccagtgggcacaat	6801
4205	TGCCATCTATAACGTTGGCCGCAACAGTTTCACCGATTCAGCCACAGACAGACAGTACCGC	4264
6802	taaaacagctcatgtgcggctcgttaccccgctcatccacgctgtagcgcctaatttctcgc	6861
4265	AAACTGACTCTGTGCCAAGAAAGAAAGTGATCCACGGGTGGCCCTGATTTCCGGAA	4324
6862	cacgactgaagcggaaggagcgcgaattggccgctgtctaccgggcagtgccgcgcga	6921
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[illegible]

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 QY 7984 gacgttcggcgaacttgcgagcagaggtcgatgctgttgcctccgggattacttcgg 8043
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 Db 6362 CGGTGAATCCCAACACTGGACTCAGCGACATTCAGGTTGAATGCTTCGNAATATGCG 6421
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RESULT 8

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 Db 6602 AGACGTGAAAAGTTACACTGGCAGCAAAACACACAGAGAAAGAACCCGAAAGTACAAAGTAT 6661
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Db 1391 CCCAGCCCTCTTTTACGCGCTTTCCCATGTCATCCGTAAGACTACCTCTTTGCCCATGTC 1450
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[illegible]

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Qy	7579	ggtaacctcagttggttagtcgcgcgaagtatgcgcgcatctacgcggaacacatcagatcg	7638
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Qy	7639	gtcgttac-----gagggtttgacttgactgacccgcgcgactgctctccacitgcagcaga	7695
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Qy	7834	cgcagacacatgtggaacctcgagaaccgactctccaccgcgcgcgaagagagc-----	7888
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Qy	8119	acaacaaaaatccgttaggcagcaaatctccagtgcgcaaatggatcggtccacgga	8178

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RESULT          9
US-08-801-263A-7
: Sequence 7, Application US/08801263A
: Patent No. 5811407
: GENERAL INFORMATION:
: APPLICANT: Johnston, Robert E.
: APPLICANT: Davis, Nancy L.
: APPLICANT: Simpson, Dennis A.
: TITLE OF INVENTION: System for the In Vivo Delivery and
: TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
: STREET: 1211 East Morehead Street
: CITY: Charlotte
: STATE: No. 5811407th Carolina
: COUNTRY: USA
: ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,263A
 FILING DATE: 19-FEB-1997
 CLASSIFICATION: 51A
 ATTORNEY/AGENT INFORMATION:
 NAME: Sidley, Kenneth D.
 REGISTRATION NUMBER: 31,665
 REFERENCE/DOCKET NUMBER: 5470-147
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-420-2200
 TELEFAX: 919-881-3175
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11663 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 08-801-263A-7

Query Match	14.6%	Score 2271.2	DB 2	Length 11663
Best Local Similarity	58.3%	Prod. No. 0		
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 6182 AGACGGGACAGTGGCTTGCCTTAGTACTGCAACTTTTGGCCCGCAAGCTTAGAGTTA 6241
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Query Match	14 68;	Score	2271.2;	DB 5;	Length	11663;
Best Local Similarity	58.3%;	Pred. No. 0;				
Matches 4384;	Conservative	0;	Mismatches	2893;	Indels	237; Gaps
						14;
2644	agtgcattgtgattgagcgtgacagcccatcatcaagctcttgacagagcatttc					2703
74	AGTTAACGTAGAGGTAGACCCTCAGNCTCGTTCGTGCAACGAAAGAGCTTCC					133

QY	2704	gtcgttcgaggtgagatcatctcaggtcacaccaaatgacccatgcaaaatgccagagcatt	2763
Db	134	GCATTTGAGGTAGTACACAGAGTCTACCTCAATGACCATGCTAATGCGACAGCAT	193
QY	2764	tctgcaccccttgcacaaatgatagcagagagactgacaaagacacacatcttgg	2823
Db	194	TTCCGATCTGGCCAGTAAACTATGATGAGTGGAGGTCTCTACACAGGACGATTTTGA	253
QY	2824	tatgcagatgcgtctccagagagatgatctacgcacaaataccactgogtatgcc	2883
Db	254	CATAGCAGCGCACCGGCTCGTGAATGTTTCCGAGCACAGTACCATTTGGTTGGCC	313
QY	2884	tatgcagcgcagagagacccccgaaaggctcgatagctacgcaaaagaaactgcagcgc	2943
Db	314	CATCGGTAGTCCAGAGACCGGACCGCATGATGAATATGCCAGCAAACTGGCGAANA	373
QY	2944	ctcgcggaaggctggtatagagagatcgaggaataacacgcactgcagacccgat	3003
Db	374	AGCATGTAAAGATTACAACAAAGAACTTGCATGAGAGATCAAGGACCTCCGGACCTACT	433
QY	3004	ggctacgcagacgtgaatctctacatttgcctgcatacagagactcagctgctgac	3063
Db	434	TGATACACCGGATGCTGAAGCCCATCACTGCTCTCCACAAAGATTTACCTTGCAACAC	493
QY	3064	ggcagccgaagtggcgtatataccagagctgtatgctgtacatgcacacacatcgtgta	3123
Db	494	CGGTGCCGAGTACTCCGTCATCGAGAGCTGTA--CATCAACGCTCCGGAACTATTTA	550
QY	3124	ccatcagcgcagatgaaggctcagaaacgctgattggattgggtttgacacacccggt	3183
Db	551	CCACAGGCTATGAAGCGTGGGACCGCTGTACTTGGATTGGCTTCGACACACCCAGTT	610
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QY	3244	ggtgtacagcgcagaaacataggaactgtgtcagcatcttgaactgaggaagactcgg	3303
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QY	3304	caaaactgtccatctccgcaagaagaactgaaacctgtgcacacagtcatttctcgt	3363
Db	731	AAAGTTCTCGATATGAGGAAGAAGGATGAGCCCGGGTCACGGGTTTATTTCTCGT	790
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QY	3484	aggttacgtagttaagaaaatcactatgtgcccggcgtgtacggttaaacgtaggta	3543
Db	911	AGGTACCTAGTGAAGAAATCAACATCAGTCCCGGGATCACGGGAAACCGTGGATA	970
QY	3544	gcctgtacgtatcacgcggaggttccgtgtgtgaaagccacagacactgtcaagg	3603
Db	971	CGCGGTTAAACAAATACGAGGGCTCTTGTCTATGCAAAAGTTACCGATACAGTAAAGG	1030
QY	3604	agaaagagttctattccctgtatgcacctaogtccccccaacctctgtatcaaatgac	3663
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QY	3664	tggtacactagcagcagcctcacacggagagcagcagagaagttgttagtgggattgaa	3723
Db	1091	CGGCATATAGGCCACCGGATATCTCACCTGACCATGCAACAAAACCTCTGGTTGGCTCAA	1150
QY	3724	tcagaggtatgttggaaacggaagaacacagcgcgaacactaacagatgagaactact	3783
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[illegible]

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Db 6722 CAGGCTTACAGCGCTTTTGCTACCCACATTCACACGCTCTTTGACATGTCGGCGGAGGA 6781
Qy 9139 ctttgacgcgatcatcgctctcactccaccacagagagaccgggttctagagacggacat 9198
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Qy 9559 gattcattgacgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 9618
Db 7202 GATCATTTAGCGCATCTATCGGCGAGAGACACCTTACTTCTCGGTGGATTTCATCTTGA 7261
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Db 7262 AGATTCGGTTTACCTCCACAGCGTGTGCGCTGGCGGACCCCTTGAAGAGCTGTTAAGTT 7321
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RESULT 11

US-08-801-263A-4

: Sequence 4, Application US/08801263A

: Patent No. 5811407

: GENERAL INFORMATION:

: APPLICANT: Johnston, Robert E.

: APPLICANT: Davis, Nancy L.

: APPLICANT: Simpson, Dennis A.

: TITLE OF INVENTION: System for the In Vivo Delivery and

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: TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
: STREET: 1211 East Morehead Street
: CITY: Charlotte
: STATE: No. 5811407th Carolina
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/801,263A
: FILING DATE: 19-FEB-1997
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Sibley, Kenneth D.
: REGISTRATION NUMBER: 31,665
: REFERENCE/DOCKET NUMBER: 5470-147
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-420-2200
: TELEFAX: 919-881-3175
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11717 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-801-263A-4

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Query Match 14.3%; Score 2224.4; DB 2; Length 11717;
Best Local Similarity 58.2%; Pred. No. 0;
Matches 4401; Conservative 0; Mismatches 2876; Indels 291; Gaps 16;

QY 2644 agtgcattgtgttatgtaggctgacagcccttcatcaagctttgcagagagcatttcc 2703
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Db 134 GCAATTTGAGGTAGTACGACAGCAGGTCACTCCAAATGACCATGCTAATGCCAGAGCAT 193
QY 2764 ttgcgcactggtctaccacaaattgacgcagcagagactgacacaaagacacactctcttga 2823
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RESULT 12
 US-09-102-248-4
 : Sequence 4, Application US/09102248
 : Patent No. 6008035
 : GENERAL INFORMATION:
 : APPLICANT: Johnston, Robert E.
 : APPLICANT: Davis, Nancy L.
 : APPLICANT: Simpson, Dennis A.
 : TITLE OF INVENTION: System for the In Vivo Delivery and
 : NUMBER OF SEQUENCES: Expression of Heterologous Genes in the Bone Marrow
 : NUMBER OF SEQUENCES: 12
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
 : STREET: 1211 East Morehead Street
 : CITY: Charlotte
 : STATE: No. 6008035th Carolina
 : COUNTRY: USA
 : ZIP: 28234
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/102,248
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/801,263
 : FILING DATE: 19-FEB-1997
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Sibley, Kenneth D.
 : REGISTRATION NUMBER: 31,665
 : REFERENCE/DOCKET NUMBER: 5470-147
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 919-420-2200

Query Match	14.3%;	Score 2024.4;	DB 5;	Length 11717;	
Best Local Similarity	58.2%;	Pred. No. 0;	Mismatches 2876;	Indels 291;	Gaps 16;
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134	GCAATTTGAGGTAGTAGCACACGACGAGTCACTCCAAATGACCATGCTAATGCCAGCATT	193			
QY 2764	ttcgcaacctggctacaaattgatcgagcaggagactgacaaagacacactcatcttggg	2823			
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194	TTCCGATCTGGCCAGTAAACTAATTCGAGCTGGAGTTCTTACCACAGCGAGATTITGGA	253			
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Db					
254	CATAGCCAGCGACCCGGCTGTAGAAATGTTTCGAGCACCATGACCATTTGCGCTTGGCC	313			
QY 2884	tatgcccagcgcagaagacccccgaaagcctcgatagctacgcgcaaaagaaactggcagcgc	2943			
Db					
314	CATCGGTAGTCCAGAAACCGGACCGCATGATGAATATGTCGCAACTGCCGAAAAA	373			
QY 2944	ctccgggaagtgctgatatagacagatcgacagaaaataccacgacctgcagacgctcat	3003			
Db					
374	AGCATGAAGATTACGAATTAAGAACTTGCATGAGAAGATCAAGAGACTCCGACCGTACT	433			
QY 3004	ggctacgccagcgtgaaatctcctacctttgctgcgtacacagcgtcacgctgctgac	3063			
Db					
434	TGATACACCGGATGCTGAACGGCATCACTGCTTCCACACGATGTTACTCTGCAACAC	493			
QY 3064	ggcagccgcaagtgccgatatcaggagcgtgatcgtgtacatgcaccaacatcgtctga	3123			
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Db					
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Db					
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QY 3244	ggtgttacagggccaggaacataggaactgtgacgactccttgactgagggagactcgg	3303			
Db					
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QY 3364	aggatctacattgtacactgagacagaagactactgaggagtggtgcacttaccctccgt	3423			
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791	TGGATCGACACTTATCCCGAGAACACAGAGCCAGCTTGCAGAGTGGCATCTTCCATCGGT	850			
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Db					
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QY 3484	agggtagctagttaaagaaatcactatgtgccccgcctgtacggttaaaacagtgaggta	3543			
Db					

RESULT 12
US-03-12-248-4
Sequence 4, Application US/09102248
Patent No. 6008035
GENERAL INFORMATION:
APPLICANT: Johnston, Robert E.
APPLICANT: Davis, Nancy L.
APPLICANT: Simpson, Dennis A.
TITLE OF INVENTION: System for t
TITLE OF INVENTION: Expression o
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park &
STREET: 1211 East Morehead Str
CITY: Charlotte
STATE: No. 6008035th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,2
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/801,2
FILING DATE: 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200

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1751	Db	CATCGTTGTCTCGCCAACTCTGCTGTGAAGACGCTAACTCGCACACAGCACCCGCT	1810
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1811	Db	AGCAGACCCNGTTAAGATCATACGCACTCCGGAAGATCAGGAAGGTATGCAATCGAACCC	1870
4435	Qy	atatgacggcaggggtcctaactacatgtgatcgccatctccggtccctgtagtttcaagc	4494
1871	Db	ATACGAGCTTAAATGACTGATGCCAGCAAGATGCGGTACCATGCCAGAATCTTAGC	1930
4495	Qy	tttagcgcagagcgcactacttggtgtacaacgaaagggagttgtcaacagagaactata	4554
1931	Db	ACTGAGTGAGAGCGCCAGCTAGTGTGTACAACGAAAGAGATTTGTGAACCGCAAGCTGA	1990
4555	Qy	ccatattgcggttcacgacgcgtcgtgcauccacgcagaggaactacagagaaagtcag	4614
1991	Db	CCATATTGCCATGCAAGTCCCGTCCGCTTGAATACAGAAAGAGGACGATACAAAGGTTACAAA	2050

4615	QY	agctgaagaactgacccagtagctggttcgacgtagataaaaaatgctgcgtcaagag	4674
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4675	QY	agaggaecgtcggtgttgggttgggtgggagagctaaaccaaccccccttccatgaatt	4734
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4735	QY	cgcctacgaaggctgaagatcagcgcgctcggcaccataataagactacagtagaggagt	4794
2171	Db	agctcttggaggactggaagactgcaccctgggtcccgctacaaggttgaaacaaataggagct	2230
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4855	QY	tctggttcacagcggcaagaagaagaaactgcagagaaatagttaacgacgtgaagaagca	4914
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QY	7835	gcagaccatgtggacctcgaaaccca-----ttctctcc	7869
Db	5405	GGCAAGAATACGAGGAAGAGCCAACTCCACCGCAAGCACCAGCTCTCGGAGCAGTCCCT	5464
QY	7870	acgcgccgaagagagctgcataccttgctcccgcgcgcgagcgagacggtgcgcgc	7929
Db	5465	TCACCTTCTTTGGTGGGTATCCATGTCCTTCGGATCCCTTTTCGACGGGAGAGATGG	5524
QY	7930	gccggaagaacgagcctgcgccaagactgcgttttaggaacaagotgccttgcagctt	7989
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QY	7990	cggcgactttgacgagcaacgagtgatgcgttgccctccgggattactttcggagactt	8049
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Db	5645	CGTCCCTGTTGGGTCAATTGAACCGGGCGAAGTGAACATATATATGTCGCCGATCAGT	5704
QY	8054	-----gacgtctctgcg	8064
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QY	8125	aaaatccgttaggcagcaaatctccagtcgcacaactgtagcggtccaggagagaa	8184
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QY	8185	aatgtaccgcgcaaaattggatactgagaggagaaagctgttgcgtcgaaatgcagat	8244
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QY	8245	gcacccatcgagggttaataagatcgataccagcttcgcaagtggagacaatgaagc	8304
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QY	8425	attctcaagccccgattagcaatcgacgctggaacgaatacctatccagaattacc	8484
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QY	8605	acatcatcgTaccaccagcgactgtacgcagtcgcgtcccgctccacccttcagaacac	8664
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QY	8905	cttggttcgcgtcgcagggggttcccatggacagattcacggtgcacataaaacgagatgt	8964
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QY	8965	caaatcactccggagacgaacacacagagagaagaccccaaatccaggtaatccaagc	9024
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Db	6722	CGCAGAACCCCTGGCAGCCGCTTACCCTGTCGGGATCCACCGGAGTTAGTTCGACGGCT	6781
QY	9085	aaatgctgtgttagcgcctaaagtcacacatatgtttgatattgtcggccgaagacttga	9144
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QY	9145	cgcgatacgcctctcaactccaccagagacccgggtcttagagacggacattgcatc	9204
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QY	9205	attcgacaaaagccagagacactccttggctcttacagtttaagtatcctcgaagatct	9264
Db	6902	GTTCGACAAAAGCCAAGACACGCTATGSGCGTTAACTGGCTGNTGATCTTGGAGACCT	6961
QY	9265	aggggtgatcagtlactcgtcgtgacttgatcgagcgacctttggggaaatatccagctg	9324
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QY	9325	tcacctaccaactgcgcgcgcttcaagtlcgagctatgatgaatcgggcattgtct	9384
Db	7022	CCATCTGCCACGGTACCCGTTTCAATTCGGGGCCGATGATGAATTCGGAATGTTCCT	7081
QY	9385	gactttgtttataactgtttgaaacatcaccatcgcaagcaggggtactcgacagag	9444
Db	7082	CAGCTCTTTGTCAACACAGTCTCTGAATGTCTGTTATCGCCAGCAGAGATTTGGAGGAGCG	7141
QY	9445	actcactgactcgcgcgttcgcgccttcactcggcgacgaacacatcgttcacggagtcat	9504
Db	7142	GCTTAAACGTCCTCAATGTGCAGCATTTATCGCGCAGCACAACATCATACACGGAGTAGT	7201
QY	9505	ctcgcacagctgatggcgagaggtgcgcgtcgtgggtcaacatgaggttgaagatcat	9564
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QY	9565	tgaactgtcatggcgaaaaacccccatttttggggggattccatagttttgacag	9624
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QY	9625	cgtcacacagcgcctgcgtgttttcagaccacactaaagccctgttcaagttgggtaa	9684
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QY	9685	cccgttaacagctgaagacaagcagcagacgagacagcggcgacactgagtgacaggt	9744
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QY	9745	tagcaagtgtttccgacagcgttggtgggcgaactggaggtggccactcaactctaggtta	9804
Db	7442	AAAGCGCTGGTTTAGATAGTAGGTATTAACAGACACCTTAGCAGTGGCGTGGCAACTCGTGA	7501

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Qy	6085	tgagtaacagcgggttaaaggcagtaggggttagctggctggtcaataaagtaagagggtta	6144
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Db	3608	CTCAGTACTTGTGGTATCATCAGAGGAAAAAATTTGAAGCTCCCGTAAGAGATCGNATGGAT	3667
Qy	6205	gtaccgctgaattgtcacagggcccgataggtgctacacactaagtatttaggaactgcggc	6264
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Qy	6325	ctaccagcagtggtgcaccaccccatgaagctgcagatgcttgggggagatgcgtacg	6384
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Qy	6385	actgctaaacccggcgga---tcttgatgagagcttaagatagcgcgataaaatcag	6441
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Qy	6859	tgccagactgaagcgggaaggggaccgcgaatttggcgcgtctetaccggcagatggcgc	6918
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RESULT 14
US-09-102-248-8
; Sequence 8, Application US/09102248
; Patent No. 6008035
; GENERAL INFORMATION:
; APPLICANT: Johnston, Robert E.
; APPLICANT: Davis, Nancy L.
; APPLICANT: Simpson, Dennis A.
; TITLE OF INVENTION: System for the In Vivo Delivery and
; TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
; NUMBER OF INVENTIONS: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Bell Seltzer Park & Gibson, P.A.
; CITY: Charlotte
; STATE: No. 6008035th Carolina
; COUNTRY: USA
; ZIP: 28234

```


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Sun Feb 13 13:44:47 2000

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RESULT 15
US-08-741-881-1
; Sequence 1, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741.881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-6031
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16656 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-741-881-1

Copied from 09549937 on 04/17/2006

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 Db 2471 CTTGATTTGCTATGCTCAGGCGCGCAGGAAGTAGTACTATGCGGAGCCCATGCAATG 2530
 Qy 5095 cggattctcaatatgatgcagcttaagtgaacttcaaccac-----aacatctg 5145
 Db 2531 CGGATTTCAACATGATGCAACTAAGGTACATTTCAATCACTCCCTGAAAAAGACATATG 2590
 Qy 5146 cactgaagtatgcataaaagtataccagagcttgcacgctccagtcacgcccagctcgt 5205
 Db 2591 CAGCAAGACATTTACAACTATATCTCCCGGCTTGCACACAGCCAGTTACAGCTATTGT 2650
 Qy 5206 gtctagcttcactaagagggcgaagtgcacagcaaccccgctgcaacaaacccataat 5265
 Db 2651 ATCGACACTGCATTACATGGAAGATGAACACACCCGCTGCAAGAAGAACATTGA 2710
 Qy 5266 catagacacacaggaagacagaccagccagcagagacatcgtgttaacatgctccg 5325
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 Qy 5386 atctcagggctcaccgcgaaggggtatagccgctgaagcagaaggtgaatgaataac 5445
 Db 2831 CTCACAGGGCTAACACAGAAAGAGTGTATGCGCTCCGCGCAGAAAGTCAATGAACACC 2890
 Qy 5446 cttgtatgcccctcgtcgagcagcgtgaatgactgtgacgcgactgagtaggct 5505
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 Qy 5506 ggttggaaaacgctggcggcgatccctgattaaaggtcctatacaaacattccacaggg 5565
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 Qy 5566 taacttacggccacatttgaagaaatggcaagaagaacagacaaataatgaaggtgat 5625
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 Qy 5626 tgaagcagcggctgcgctgtggacgcttccagaaacaaagcgaactgtgttggcgaa 5685
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 Qy 5686 aagcctggtgctgctctggaactcgcgggaatcagatgacagcagagaggtgagcac 5745
 Db 3131 AGCATTTGGAACCGATACCTAGCCACGCGGATTCGTTACTTACCGGTGCCAGTGGAGGA 3190
 Qy 5746 cataattacagcatttaagagagcagagcttactctcagtggtggccttgaatgaat 5805
 Db 3191 ACTGTTCCACAGTGTTCGGATGACAAACCACTTCGGCCATTTACGCCCTTAGAGTAA 3250
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Job time: 2291 sec

Db 6539 TAGACTGAAGGCCCTAAGCGCCACACTATTTGCAAGACGTATAATTTGGTCCCAT 6598
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Db 6599 GCAGAAAGTGCCTATGGATAGATTGCTCATGACATGAAGAGACGTGAAGTTACACC 6658
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Qy 9037 ggcgaccgttacctgtgcygcattccacaggaattagtaaggagactaaatgctggtt 9096
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Qy 9097 acgcccctaagctgcacacatgtttgatgtcgccgaagactttgacgcgcatcgc 9156
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Qy 9217 ccagagacactccttggctcttaaggtttaaataatcctcaaatctagggggatca 9276
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Qy 9337 tggcagcgcttcaagttcggagctatgatgaatcgggcatgtttctgactttgttat 9396
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Qy 9517 gatggcgagaggtgcgctgtgggtcaacatgaggtgaagatcattgaogctgcat 9576
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Db 7559 CATCAGAGGGGAAATAAGCATCTCTACGGTGTCTCTAATATAGTCAGCATAGTACA 7614

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2000, 04:52:55 ; Search time 418.56 Seconds
(without alignments)
9287.759 Million cell updates

Title: US-09-190-246-1
Perfect score: 15538
sequence: 1 ttcgcgctttcgggtgatgac.....tatcacgaggccctcttcgc 15538

Scoring table: IDENTITY NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match	Ident				
1	7340	47.2	11517	1	Q26021	1	PSF6-SFV4 RNA tran
2	2987.8	19.2	4912	1	X08423		Recombinant vector
3	2962.2	19.1	4864	1	T01114		Expression vector
4	2962.2	18.1	4864	1	V21737		Vlneo sequence us
5	2959	18.0	4864	1	Q74207		Expression vector
6	2950	18.9	5898	1	V00677		DNA plasmid VR2211
7	2919.2	18.8	5843	1	V00677		DNA plasmid VR2211
8	2272.8	14.6	11663	1	V33473		South African Arbo
9	2271.2	14.6	11663	1	V33475		South African Arbo
10	2255.2	14.5	11663	1	T47568		South African Arbo
11	2224.4	14.3	11717	1	V33474		Girdwood S.A.virus
12	2222.8	14.3	11703	1	V33476		Sindbis virus clone
13	2211.6	14.2	16656	1	Q86154		Eukaryotic layered
14	2211.6	14.2	16656	1	T30787		Alphavirus-based e
15	2211.6	14.2	16656	1	V42364		Representative euk
16	2211.6	14.2	16656	1	V60125		Representative euk
17	2211.6	14.2	16656	1	V70684		Representative euk
18	2082.8	13.4	11464	1	V74108		Venezuelan equine
19	1896.2	12.2	4646	1	X19441		Expression vector
20	1804.6	11.6	4432	1	T01113		Expression vector
21	1799	11.6	4296	1	T28272		Plasmid pMH28 sequ
22	1799	11.6	4352	1	T28273		Plasmid pMH29 sequ
23	1799	11.6	6047	1	T28278		Plasmid pMH30-lux
24	1796.6	11.6	4432	1	T42026		Expression vector
25	1763	11.3	3993	1	T28277		Plasmid pMV306 seq
26	1762	11.3	4505	1	T28276		Plasmid pMV281 seq
27	1762	11.3	6171	1	T28279		Plasmid pMV261-lux
28	1762	11.3	4120	1	T64421		Plasmid pMV206. My
29	1760.4	11.3	4120	1	T28281		Plasmid pMV206 seq
30	1759.8	11.3	6044	1	T28280		Plasmid pMV361-lux
31	1759.8	11.3	11492	1	T74107		Western equine enc
32	1754	11.3	4120	1	Q21502		Vector pMV206 for
33	1708.2	11.0	4119	1	Q41331		pMV206 - cassette
34	1582.4	10.2	1899	1	Q29632		HRSV glycoprotein
35	1582.4	10.2	1899	1	V18735		HRSV glycoprotein
36	180.8	10.2	1899	1	N70793		Sequence encoding
37	1379.4	10.2	15222	1	T78440		Human respiratory
38	1379.2	10.2	1899	1	N90751		Sequence encoding
39	1577.6	10.2	1899	1	T04031		RS virus fusion pr

40	1574.6	10.1	15223	1	T63430	Respiratory syncyt
41	1574.6	10.1	15223	1	T63430	Respiratory syncyt
42	1571.2	10.1	15223	1	V17553	Respiratory syncyt
43	1570	10.1	4928	1	T32656	Plasmid encoding h
44	1570	10.1	3547	1	T01115	Expression vector
45	1570	10.1	13254	1	T40315	Nucleotide sequenc
46	1570	10.1	3610	1	V00659	Synthetic hepatitis

ALIGNMENTS

```

RESULT 1
Q26021
ID Q26021 standard; DNA; 11517 BP.
AC Q26021;
DE 05-JAN-1993 (first entry)
DT PSP6-SFV4 RNA transcript as DNA.
KW Semliki forest virus; SFV; SP6 expression vector; RNA polymerase; ss.
OS Synthetic.
SH key
TS Location/Qualifiers
CT 87..7379
CJ /*tag= a
CJ /label= Non-structural_polyprotein
CT 7421..11182
CJ /*tag= b
CJ /label= Structural_polyprotein
W09210578-A.
25-JUN-1992.
12-DEC-1991; SE0855.
13-DEC-1990; SE-003978.
(GIOP-) BIOPTION AB.
Garoff H, Liljestrom P;
WPI: 92-234633/28.
P-PSDB; R25138 AND R28337.
RNA mol. derived from alphavirus RNA genome - chimeric alphavirus
antigen and vaccine for immunisation against viral infections
Disclosure; Fig 5; 94pp; English.
The sequence given contains a full length Semliki forest virus (SFV)
cDNA clone within an SP6 expression vector. The SP6 RNA polymerase
promoter allows in vitro transcription of full length and infectious
transcripts.
Sequence 11517 BP; 3130 A; 2985 C; 3091 G; 2311 T;

```

Query Match	47.2%	Score 7340;	DB 1;	Length 11517;
Best Local Similarity	99.4%;	Pred. No. 0;		
Matches 7379;	Conservative	0;	Mismatches 40;	Indels 5; Gaps 1;
QY 2548	atggggatgtgtgacatacacgacgacgacgaagattttgtccagctctctgcacctccg	2607		
Db				
2	ATGGCGGATGTGTGACATACAGGACGACCAAAAGATTTGTTCAGCTCTCTGCCACTCCG	61		
QY 2608	ctacgcgagagattaacaccaccagatggcgccaaagtgcattgtgatattgaggctga	2667		
Db				
62	CTACGCGAGAGATTAAACACCACGATGGCGGCCAAAGTCATGTGTGATNTGAGGCTGA	121		
QY 2668	cagcccatctcaagtcctttgcagaagcattccctgcgttcgtagggtagctatgca	2727		
Db				
122	CAGCCCATCTCAAGTCTTTTGCAGAAAGCATTTCCGTCGTTCGAGGTGGAGTCATTGCA	181		
QY 2728	ggtcacaccaaatagccatgcaaatccagagacatttcgcacctggctaccacaaattgat	2787		
Db				
182	GGTCAACACCAATGACCATGCAANTGCCAGAGCATTTTTCCGACCTGGCTACCAAAATTGAT	241		
QY 2798	cgacgaggactgacaaagacacactcatctcttgatatacggcagtcgcgcttccaggag	2847		
Db				
242	CGAGCAGGAGACTGACAAAGACACACTCATCTTGGATATCGGCGAGTCGGCTTCCAGGAG	301		
QY 2848	aatgatgtctacgacaaataccaatgcgtatgcccttatgcgacgcgagaagaccccca	2907		
Db				
302	AATGATGTCATACGCACAAATACCACTGGTATGCCCTATCGGCAGCGCAGAACGCCCGA	361		
QY 2908	aagctcgatagctacgacaaagaaactggcagcgccctccgggaaggtgctggtagataga	2967		

[illegible]

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QY	13508	tcggttaggttcgttcgctcccaagctgggctgtgtgacgaaccccccttcagccgcag	13567
DB	2882	TCGGTGTAGTTCGTTCCCTCCAGCTGGCTGTGTGACGAACCCCGCTTCAGCCGAC	2941
QY	13568	cgtctggccttaccggttaactatcgctctggtgctcccaaccccgtaagacagactatcg	13627
DB	2942	CGCTGGCCCTTATCCGCTAACTATCGTCTTGAGTCCGCTGAGTAAAGACACACTTATCG	3001
QY	13628	ccactggcagcagccactgtaacagattagcagagcaggttatgtagcgggtgctaca	13687
DB	3002	CCACTGGCAGCAGCCACTGGTAAACAGGATAGCAGAGCGAGGTATGTAGCGGTGTCTACA	3061
QY	13688	gagctctgaagtgtgtgctcctaactcggctacactagagaacagattatgttatctgc	13747
DB	3062	GAGTCTTGAAGTGTGGCTTAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	3121
QY	13748	gctctgtgaagccagttactcttcggaaagagtggttagctcttgatcccgcaacaa	13807
DB	3122	GCTCTGTGAAGCCAGTACCTTCGGAAAGAGATGGTGTAGCTCTTGTATCCGGCAACAA	3181
QY	13808	accacccgtgtagcgtgtgtgtttttgtttgttgaagcagcagattacgcgcagaaaaaa	13867
DB	3182	ACCACCGTGTGAGCGGTGTTTTTGTGCAAGCAGCAGATTACCGCAGAAAAAAA	3241
QY	13868	ggatctcaagaagatccctttagctttttctacgggtctgacgctcagtggaacgaaac	13927
DB	3242	GGATCTCAAGAAGATCCCTTGTATCTTCTACGGGGTCTGACGCTCAGTGAACGAAAC	3301
QY	13928	tcacttaagggatttggctgatgatgatattcaaaaaggatcttcaactagatcccttta	13987
DB	3302	TGACGTTTAAAGGATTTGGTCATGAGATTATCAAAAAGGATCTTCACTAGATCTTTTA	3361
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DB	3362	AATTAAAAATGAAGTTTAAATCAATCAATGATATATGATGATTAACCTGCTTCAGCT	3421
QY	14048	taccaatgttaactcagtgagcaccatctctcagcagctctcttattctgttccatcata	14107
DB	3422	TACCAATGCTTAATCAGTGAGCACCATTCTCAGCGATCTGCTATTTCTGTTCCATATA	3481
QY	14108	gttgctgactcgggggggggggggggctgaggtctgctcgtgtaagaaggtgttgcag	14167
DB	3482	GTTGCTGACTCGGGGGGGGGGGGGGGCTGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCT	3541
QY	14168	tcatacaggctgaatcccccacatcatcagccgaagaagtgaagggccagcgggtgatg	14227
DB	3542	TCATACAGCCCTGATTCGCCCATCATCCAGCCAGAAAGTGAGGGAGCCAGGTTGATG	3601
QY	14228	agagcttgggttaggtggaccagttgggtatttgaactttgttgcacggaacgg	14287
DB	3602	AGAGCTTGGTGTAGGTGGACCAAGTTGGTGAATTTGAACCTTTTGGCTTCCACGGAACGG	3661
QY	14288	ctcgtgtgctgggaagatcgtgactgctgctcctcaactcagcaaaagtctgattatt	14347
DB	3662	TCTCGGTGCGGAAGATCGGTGAICTGATCTTCACTCAGCAAAAGTTCGATTTAT	3721
QY	14348	caaaaagccgcctcccgctcaagtcagtcagcgttaatgctctgcaggtttcaaccaattaa	14407
DB	3722	CAACAAGCCCGCTCCCGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG	3781
QY	14408	ccaattgtagtagaanaaacatcagacatcaaatgaactcaaatatttattcatatcag	14467
DB	3782	CCAATTGTGTAGTAAAGATCTCGAGCATCAANTGAACACTGCAATTTATTTCATATCAG	3841
QY	14468	gattatcaataccattttttgaaaaagccgtttctgttaatgaaggaagaaactaccga	14527
DB	3842	GATTATCAATACCATATTTTGAAGAGCCGCTTCTGTAATGAAGGAGAAACTCACCGA	3901
QY	14528	ggcagttccatagtagcagatcctgtatcgtctgctgctgctgctgctgctgctgctgct	14587
DB	3902	GGCAGTTCCATAGGATGCAATATCTCTGTATCGGCTGCGGATCCGACGCTGCCAAT	3961
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QY	14648	gagtgacgactgaatccgctgagaaatgcaaaagcttatgattcttcttcagacttgtt	14707
DB	4022	GAGTGACGACTGAATCCGGTGAGATGGCAAAAGCTTATGCATTCTTTCCAGACTTGT	4081
QY	14708	caacagccagccatttacgctctgctcatcaaaatcactcgcgcatacaacaaacgcttatca	14767
DB	4082	CACAGCCAGCCATTACGCTCTGCTCAATAAATCACTGCATCAACCAACCGTTATTCA	4141
QY	14768	ttcgtgattcgcctgagcgaacgaatacgcgactcgtgttaaaagacaaattacaaa	14827
DB	4142	TTCTGTATTCCGCTGAGCGAGACGAATAACGCGATCGCTGTATAAAGGACAAATTACAAA	4201
QY	14828	caggaatcgaatgcaacccggcgcggaacactccagcgcatacaacaatattttccctg	14887
DB	4202	CAGGAATCGAATGCAACCCGCGCAGGAACACTGCCAGCGCATCAACAATATTTCACCTG	4261
QY	14888	aatcaggatattcttctaatcactgggaatcgtttttccggggatcgcagtggtgagta	14947
DB	4262	AATCAGGATATTCTTCTAATACCTTGGAAATGCTTTTCCGGGGATCGCAGTGTGAGTA	4321
QY	14948	accatgcatcatcaggagtagcggataaaatgcttgatggtcggaagaggcataaaatccg	15007
DB	4322	ACCATGCAATCAGGAGTAGCGGATAAAATGCTTGTGATGGTGGGAAGAGGATAAATTCGG	4381
QY	15008	tcagccagtttagtgcacatctcatctgaacatcattgcaacatcattgcaacgctaccccttgc	15067
DB	4382	TCAGCCAGTTTGTAGTCTGACCATCTCATCTGTAACATCATTTGGCAACGCTACCTTTGCCAT	4441
QY	15068	gtttcagaaacactcctggcgcatcggttcccatataaatacagcattccatgttggat	15127
DB	4442	GTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTGCGACCTG	4501
QY	15128	attgcccagacattatcgcgagcccatattatcccatataaatacagcattccatgttggat	15187
DB	4502	ATTGCCGACATATTTCGGGAGCCCATTTATACCCATATAAATCAGATCCATGTTGGAAT	4561
QY	15188	ttaactcggcctcagcaagcgtttcccggttgatggtcctataacagcttccctgtat	15247
DB	4562	TTAATCGCGGCTTCGACGAAGAGCTTCCCGTTGAATATGGCTCATAACTGCTTCTTGTAT	4621
QY	15248	tactgtttatgaagcagacagcttttattgttcacatgataataattttatctgtgcaa	15307
DB	4622	TACTGTTTATGTAAAGCAGACAGTTTATTGTTTCATGATGATATATTTTAICTTCTGCAA	4681
QY	15308	tgtaacatcagagattttgagacacaaagctgtttcccccctcccccctattattgaagca	15367
DB	4682	TGTAACATCAGAGATTTTGAGACACAACTGGCTTTCCTCCCTCCCTCCCTATTTTGAAGCA	4741
QY	15368	tttatcaggggttattgtctcatgagcggatataatttgaatgtatttagaataaataaac	15427
DB	4742	TTTATCAGGGTTATTGCTCATGAGCGGATACATATTTGAATGATATTAGAAAAATTAAC	4801
QY	15428	aaataggggttccgcgcacattttcccccgaagtgccactgagctcctaagaacacatta	15487
DB	4802	AAATAGGGGTTCCGCGCACATTTCCCGGAAAAAGTGCACCTGAGCTTAAGAAACCATTA	4861
QY	15488	ttatcagacatttaacattataaaatagggcgtatcagagggccctttcgtc	15538
DB	4862	TTATCATGNCATTAACTATATAAATAAGGGTATCAGAGGGCCCTTTCGTC	4912
RESULT	3		
ID	T01114		
AC	T01114		
DC	T01114		
DE	28-FEB-1996 (first entry)		
DE	Expression vector VJ1neo.		
KW	Polynucleotide vaccine; genetic immunization; coordinate expression;		
KW	HIV-1; AIDS; human immunodeficiency virus; antigen; immunogen;		

KW CMVIntA-GBH; vector: plasmid V1Jneo; ds.
 OS Synthetic.
 PN W09524485-A2.
 PD 14-SEP-1995.
 PF 03-MAR-1995; U02633.
 PR 07-MAR-1994; US-207526.
 PA (MERI) MERCK & CO INC.
 PI Liu MA, Perry HC, Shiver JW;
 DR WP; 95-328276/42.
 PT New poly-clonetic expression construct - for producing antigens and
 PT immuno-stimulatory gene products useful as vaccines against e.g.
 PS HIV, hepatitis, etc
 CC Example 1C; Page 96-99; 178pp; English.
 CC Vector V1Jneo (T01113) was obtd. from vector V1J (T01113) by
 CC replacement of the ampicillin-resistance gene with a neomycin-
 CC construct (T01112). The vector also contains a CMVIntA-CBH terminator
 CC genes. Insertion of HIV antigen genes into the vector allows
 CC large-scale production of polynucleotide vaccine in bacterial host
 CC cells.
 SQ Sequence 4864 BP; 1229 A; 1226 C; 1168 G; 1241 T;

Query Match 19.1%; Score 2962.2; DB 1; Length 4864;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2978; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 12553 agatctgctgctccttctagttgcagcgcattctgttggttccctccctccctccctcc 12612
 DB 1878 AGATCTGCTGCTCTAGTTGCGAGCCTATCTGTTGTTGCTCCCTCCCTCCCTCC 1937
 QY 12613 ttgacctggaagggtgcacactccactgctcttcttaataaatgaggaattgcatcg 12672
 DB 1938 TTGACCCCTGGAAGTGCACATCCCACTGCTCTTCCCTAATAAATAGGAAATGCA 1997
 QY 12673 cattctgagtagtgctcattctattctgtgggtgggtgggtgggtgggtgggtgg 12732
 DB 1998 CATTCTCTGAGTAGTGTCATCTTATTCTGGGGGGTGGGGTGGGGCAGCAGAGGG 2057
 QY 12733 gaggattgggaagacaaatagcaggcatgctggtggtggtggtggtggtggtggtg 12792
 DB 2058 GAGGATTGGGAAGACAAATAGCAGCATGCTGGGATCGGGTGGGGTGGGGTGGGGT 2117
 QY 12793 gtgctgaagaattgacccggttctctctgtggccgaagaagcaggcaccatcccttcc 12852
 DB 2118 GTGCTGAAGAATTGACCCGGTTCCTCTGCGCCAGAAAGAGCAGCAGCATCCCTTC 2177
 QY 12853 tbtgacacacctgtccacgccccctggttcttctagttccagccccactataggaactca 12912
 DB 2178 TGTGACACACCTGTCCACGCCCTGGTCTTGTAGTTCCAGCCCACTCATAGGACACT 2237
 QY 12913 tagctcaggagggtccgctcctcaatccaccgctaaagtacttggagcgctctctccc 12972
 DB 2238 TAGCTCAGAGGGTCCGGCTTCAATCCCAACCGCTAAAGTAGTCTGGAGCGGTCTCTCC 2297
 QY 12973 tccctcatcagccac 13032
 DB 2298 TCCTCATCAGCCCAACCAACCAACCTAGCTTCCAAAGAGTGGGAAGAAATTAAGCAAG 2357
 QY 13033 atagggtattaaatgagagggagagaaatgcctcccaacatgtgaggaagttaagagag 13092
 DB 2358 ATAGGCTATTAAGTGAGAGGGAGAGAAATGCCCTCCCAACATGTGAGGAAGTATGAG 2417
 QY 13093 aaatcatgaattctctcct 13152
 DB 2418 AAATCATGAATTTCTTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2477
 QY 13153 gggcgagcgggtatcagctcactcaaaagcgggttaatacgggttaatacagaatcagggga 13212
 DB 2478 GCGCGAGCGGTATCAGTCTACTCAAGCGGTAAATACGGTTATCCACAGAAATCAGGGA 2537
 QY 13213 taacgcaggaagaacatgtgagcaaaagccagcaaaagccagcaaaagccagcaaaagcc 13272

DB 2538 TAACGCAGGAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGCAAAAGCC 2597
 QY 13273 Cgcgttgctggcggtttttccataggtctccgccccctgcagcagcatcacaaaaatcgacg 13332
 DB 2598 CCGTGTGCTGCGGTTTTTTCATAGGCTCCGCCCTGAGGAGCATCAAAAATCGAGC 2657
 QY 13333 cteaagtcagagtgaggaaacccgacaggactataaagataccaggcggttttccccctgg 13392
 DB 2658 CTCNAGTACAGAGTGCGAAACCCAGAGGACTATAAAGATACCAAGGCTTTCCCGCTGG 2717
 QY 13393 aagctccctctgctcctctcctctcctggtccgacctgcgcttaccggataccctgcgcctt 13452
 DB 2718 AAGCTCCCTCGTCTGCTCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTT 2777
 QY 13453 tctccctctgggaagtggtggccttctctatagctcagcgtgtaggtatctcagttcgggt 13512
 DB 2778 TCTCCCTCTCGGAAGCGTGGCGCTTCTCAATGCTCAGGCTGTAGGTATCTCAGTTCCGT 2837
 QY 13513 gtaggtctgctcccaagctgggtgtgtgcagcaacccccctggttaagccccgcgcgtg 13572
 DB 2838 GTAGGTCTGTTCTCCAAAGTGGGCTGTGTGCACGAACCCCCCTTACGCCGCGCTG 2897
 QY 13573 cgccttatcggtaactatcgtcttgagtcacaccccgtaagacacgacttatcgccact 13632
 DB 2898 CGCTTATCCGGTAATCTATCTGTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACT 2957
 QY 13633 ggcagcagccactggtaacaggtatagcagagcaggtatgtaggcggtgctacagatt 13692
 DB 2958 GGCAGCAGCCACTGTTACACAGGATTAGCAGAGCGAGGTATGTAGCGGCTGTACAGATT 3017
 QY 13693 cttgagtggtggcctaactcagcgtacactagaagacagattttgggtatctgcgctct 13752
 DB 3018 CTTGAAGTGTGGGCTAACTACGCTACACTAGAGGACAGATTTTGGTATCTGCCCTCT 3077
 QY 13753 gctgaagcagttaccttcggaaaaagaggtgtgtagctctgtatccggaacaaaccac 13812
 DB 3078 GCTGAAGCAGTTACCTTCGGAAAGAGTTGTTGCTGTATCTGCGGCAACAAACAC 3137
 QY 13813 cgcgttagcgggtggttttttbtgttgcagcagcagattacgcgcagaaagagatc 13872
 DB 3138 CGCTGTGTAGCGGTGGTGTGTTTTTGTGTTGCAAGCAGCAGATTACGCCGAGAAAAGGATC 3197
 QY 13873 tcaagaagatccctttgatctttctacgggtctgacgctcagtggaacgaaactcacg 13932
 DB 3198 TCAAGAAGATCTTTGATCTTTCTACGGGCTGTACGCTCAGTGGAAACAACTCAGC 3257
 QY 13933 ttaagggtatttggtcatgagattatacaaaaggatcttcaactagatccttttaatta 13992
 DB 3258 TTAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTA 3317
 QY 13993 aaaaagaagtttttaataatcaatcaagtatataatgataaacttggtctgacagttacca 14052
 DB 3318 AAAATCAAGTTTAAATCAATCTAAGTATATATGAGTAAACTTGGTCTGACAGTTACCA 3377
 QY 14053 atgcttaactagtgagcaccctatctcagcgtatctgtatcttcttccatccatagttgc 14112
 DB 3378 ATGCTTAATCAGTGAGGCAACCTATCTCAGCGATCTGCTATTTCTGTTCCATCTAGTTGC 3437
 QY 14113 ctgact-cggggggggggggcgctgaggtctgcctcgtgaagaaggtgtgtgactcat 14171
 DB 3438 CTGACTCCGGGGGGGGGGCGCTGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3497
 QY 14172 accagcctgaatcgcccccatccacccagcaagaagtgaggagccacggttatgagag 14231
 DB 3498 ACCAGCCTGAATCGCCCATCATCCAGCAGAAAGTGAAGGAGCCACGGTTATGAGAG 3557
 QY 14232 cttgttgtagtgagaccagttggtgattttgaactttgtcttggccaggaacggtctg 14291
 DB 3558 CTTTCTGTAGTGGACAGTTGTTGATTTTGAACCTTTTCTTGTCCACGGAACGGTCTG 3617
 QY 14292 cgttgtcgggaagatcggtgatctgacctcactcagcaaaagttcgtatttattcaac 14351
 DB 3618 CGTGTGCGGAAGATCGTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 3677

[illegible]

Db 2118 GTGCTGAAGATTGACCCGGTTCCTTGGCCAGAAAGACGAGCACATCCCTTC 2177
QY 12853 tctgacacacccctgtccacgcccctgggtctttagttccagcccaactcatagacactca 12912
Db 2178 TGTGACACACCCCTGTCCACGCCCTGTGTCTTAGTTCACGCCCACTCATAGACACTCA 2237
QY 12913 tagctcagaggggtccgcttcctcaatcccacccgctaaagtacttggagcgggtctctccc 12972
Db 2238 TAGCTCAGGAGGGTCCGGCTTCAATCCCAACCGCTAAAGTACTTGGAGGGGTCTCC 2297
QY 12973 tccctcatcagcccaacaaacccaaacccctagctcccaagagtggaagaattaaagcaag 13032
Db 2298 TCCCTCATCAGCCCAACCAACCAACCTAGCTTCCAAAGTGGGAAGAATAAAGCAG 2357
QY 13033 atagctcttaagtgcagagggagagaaatgctctcccaacatgtgaggaagtaagtagag 13092
Db 2358 ATAGGCTATTAGTGACGAGGAGAGAAATGCTCCACATGTGAGGAAGTAATGAGAG 2417
QY 13093 aaatcatagaatttctccgcttcctcgtctcaactgactcgtcgtcgtcgtcgtcgtc 13152
Db 2418 AAATCATAGAAATTTCTCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCG 2477
QY 13153 gcggcagcgggtatcagctcactcaagcgggttaacgttattccacagaaatcagggga 13212
Db 2478 GCGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGA 2537
QY 13213 taacgcaggaagaacatgtgacaaagccagcaaaagccaggaacccgttaaaagcc 13272
Db 2538 TAACGCAGAAAGACATGTAGCAAAAGGCGCAGCAAAAGCCAGGAACCCGTAAAGGC 2597
QY 13273 cgcgttgctgggttttccataggtctccgccccctgacagagcatcacaaaaatcagc 13332
Db 2598 CCGCTTGTGGGGTATTTCCATAGCTCCGCCCCCTCAGCAGCATCACAAAATCAGC 2657
QY 13333 ctcaagtcagaggtggcgaacccgacagagactataaagataccagcgtttcccccctgg 13392
Db 2658 CTCAAGTCAGAGTGGCAAAACCCGACAGGACTATAAGATATACGAGCGTTTCCGCC 2717
QY 13393 aagctccctcgtcgtcctctgttccgacctcgcctcgcctcgcctcgcctcgcctcgc 13452
Db 2718 AAGCTCCCTCGTGTGCTCTCTGTTCGAGCCCTGCGCTTACCGGATACCTGTCCGCC 2777
QY 13453 tctccttcgggaagcgtggcgtttctcactagctcagctgtaggttatctcagttcgg 13512
Db 2778 TCTCCCTTCGGGAAGCGTGGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCGT 2837
QY 13513 gtaggctcgtcccaagctggcgtgtgtgacgaaccccgcttcagcccgacgcgtc 13572
Db 2838 GTAGGTGCTTCCGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAAGCCGCGCTG 2897
QY 13573 cgccttatccggttaactatcgtcttgagtcacaccccggttaagacagacttatcgccact 13632
Db 2998 CGCCTTATCCGGTAACATATCTGTTAGTCCAAACCCGGTAAGACAGACTTATCCCACT 2957
QY 13633 ggcagcgcactggttaacaggtatgacagagcaggtatgtaggcgtgtgtacagagt 13692
Db 2958 GGCAGCAGCCACTGTTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGAGT 3017
QY 13693 cttagaggtggccttaactaagcgttactactagaagaacagttattgtgtatctgcgtct 13752
Db 3018 CTTGAAGTGGTGGCTTAACCTAGCGCTACACTAGAAGGACAGTATTGGTATCTCGCTCT 3077
QY 13753 gctgaagccagttaccttcggaagaggttggtagctcttgatccggtcaacaaacac 13812
Db 3078 GCTGAAGCAGCTTACCTTCGGAAAGAGTGTGTAGCTCTTGTATCCGCAAAACCAAC 3137
QY 13813 cgtgtgagcgtggtttttttgttgcagcagcagatcagcgcagaaaaaagatc 13872
Db 3138 CGCTGTAGCGGTGTTTGTGTTTGTGCAAGCAGCAGATTACGGCGCAGAAAAAAGGATC 3197
QY 13873 tcaagagatccttgaatcttttctacgggtctgacgctcagtggaacgaaactcag 13932
Db 4278 TGCATCATCAGGATGAGGATATAATCTTGTGTTGGTGGGAGGAGGATATAATTCCTCG 4337

Db 3198 TCAAGAAAGATCCTTTGATCTTTTCTACGGGGTCTGAGCTCAGTGAAAGAACTCAG 3257
QY 13933 ttaaggatcttgggtcagtagagattcaaaaagatcttcaactagatctctttaaatta 13992
Db 3258 TTAAGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACTAGATCTCTTAAATTA 3317
QY 13993 aaatgaagttttaaatcaatcctaaagtatatagagtaaaacttggtctgacagtca 14052
Db 3318 AAATGAAGTTTTAAATCAATCTAAAGTATATATGATTAATCTGCTGACAGTTACCA 3377
QY 14053 atgcttaactcagtgagggacccttatcagcgtatcttcttcttcttcttcttcttct 14112
Db 3378 ATGCTTAATCAGTGCAGGCCTATCTCAGCATCTGCTATTTCTGTTTCATCATGTTGC 3437
QY 14113 ctgact-cg9ggggggggggcgtgaggtctcctcgtggaagaaggttctgactcaat 14171
Db 3438 CTGACTCCGGGGGGGGGGCGCTGAGGTCTGCCCTGCTGGAAGGTTGCTGACTCAT 3497
QY 14172 accagcctgaatcgcccccatcatccagccaaagtggagggagccagcgttgcagag 14231
Db 3498 ACCAGGCCCTGAATGCCCCCATCATCCAGCCAAAGTCAGGAGCCAGGTTGATGAGAG 3557
QY 14232 cttgtgtgtagtgagcaggttggtgatttggaacttttgcttgcacggagcgtctg 14291
Db 3558 CTTTGTGTAGTGCAGCAGTGGTGTGATTTTGAACCTTTGCTTTGCCACGGAACGGTCTG 3617
QY 14292 cgttgcgggaagatgcgtgactcgtcgtcctcaactcagcaaaagtctgatttcaac 14351
Db 3618 CGTTGTCGGGAAGATGCGTGATCTGATCTTCAACTCAGCAAAAGTTCGATTATTCAAC 3677
QY 14352 aaagccgcgtcccgctcaagtcagcgttaagtctcgtcgtcgtcgtcgtcgtcgtcgtc 14411
Db 3678 AAAGCCGCGCTCCGCTCAAGTCAGCGTAAGTCTGTCAGTGTAGCAACCAATTAACCA 3737
QY 14412 ttgtgattagaaaaactcctcagcactcaaatgaaactgcaattttatcatatcagagt 14471
Db 3738 TTTGATTAGAAAAAATCATCGAGACTCAAAATGAAGTTCGCAATTTATTCATATCAGGAT 3797
QY 14472 atcaataccatattttgaaaaagcgttctcgtatgaaggagagaaaaactcaccggca 14531
Db 3798 ATCAATACCATATTTTGAAGAACCGCTTCTGTAATGAAGGAGAAAACTCACCAGGCA 3857
QY 14532 gttccatagatggcagatccgtggtatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 14591
Db 3858 GTTCCATAGATGCAAGATCCTGATCGGTTCGGTTCGGATTCGGACTGCTCAACATCAAT 3917
QY 14592 acaactatttaattccctcgtcaaaaaaaggttatcaagtgaagaatcaccatgagt 14651
Db 3918 ACAACCTATTATTTCCCTCGTCAAAAAATAAGTTATCAAGTGAGAAATCACCATGAGT 3977
QY 14652 gacgactgaatccggtgagaatggcaaaagcttatgcattttttccagacttgcctaac 14711
Db 3978 GAGCACTGAATCCGTTGAGAAATGGCAAAAGCTTATGCAATTTCTTCCAGACTTGTTCAC 4037
QY 14712 agccagcattacgctcgtctcatcaaaatcactcgtcatcaacccaaacccgtttatccg 14771
Db 4038 AGCCAGCCATTACCGTCTCATCAAAATCACTCGCATCAACCAACCGTTATTCATTCG 4097
QY 14772 tgattgcgctcgtgagcagcaaatcagcgtatcgtgttaaaaggacaattacaaacag 14831
Db 4098 TGATGCGCCTCAGCGAGACGCAATACCGGATCGCTGTGTAAGGAGCAATTTACAAACAG 4157
QY 14832 aatcgaatgcaaccggcaggaacactgcccagcgcagcgcacatattttcacctgaatc 14891
Db 4158 AATCGAATGCAACCCGCGCAGCAACACTGCGCAGCGCATCAACATATTTTCACTGAATC 4217
QY 14892 aggatctcttcaatcaggaatcgtgttttcccggtggtcgtcgtcgtcgtcgtcgtcgtc 14951
Db 4218 AGGATATTTCTTAATACCTGGAATGCTGTTTCCCGGGATCGCAGTGTGTGATTAACCA 4277
QY 14952 tgcatacatcagagtaggataaaatcgttgcgttcgttcgttcgttcgttcgttcgttcgt 15011
Db 4278 TGCATCATCAGGATGAGGATATAATCTTGTGTTGGTGGGAGGAGGATATAATTCCTCG 4337

SQ	Sequence	4864 BP;	1229 A;	1226 C;	1168 G;	1241 T;
QY	15012 ccagtttagtcgaccatctcatctgtaacatcattggaacgctacaccttgccatgttt	19.0%; Score 2959; DB 1; Length 4864;				
Db	4338 CCAGTTTAGTCTGACCATCTCATCTGTACATCATCTGGAAGCTACCTTTGCCATGTTT	Best Local Similarity 99.6%; Pred. No. 0;				
QY	15072 cagaacaactctggcgactcggtctccatcacatcgaatgatgctgacactgattg	Matches 2976; Conservative 0; Mismatches 10; Indels 1; Gaps 1;				
Db	4398 CAGAAACACTCTGGCGCATCTGGCTTCCATACATCATAGATTGTGCACTGATTG					
QY	15132 cccgacattatcgcgaccattatataccatataaatacagcatcatttggatttaa					
Db	4458 CCCGACATTATCGCGACCCCATTTATACCCATATAATCAGATCATCTGTGGAATTAA					
QY	15192 tcgcgctcgagcaagactgttccgttgaatatgctcacaacgcttccctgtattact					
Db	4518 TCGCGGCTCGAGCAACGCTTCCCGTTGAATATGGCTCATACACCCCTTGTATTACT					
QY	15252 gtttatgtaagcagacagttttattgttcgatgatataattttcttgagcaatgta					
Db	4578 GTTATATGTAAGCAGACAGTTTATTGTTCATGATGATATATTTTATCTGTGCAATGA					
QY	15312 acatcagagatttgagacacacgctgttccccccccccccccattattgaagcattta					
Db	4638 ACATCAGAGATTGTGAGACACAGCTGGCTTCCCGCCCGCCCATTTATTGAAGCATTTA					
QY	15372 tcagggttattgtctcatgagcgatacatatttgaatgattattagaaaataaacaat					
Db	4698 TCAGGGTTATTGTCTCATGAGCGGATACAVATTTGAATGATTTATTAGAAAATAAACNAAT					
QY	15432 aggggttcgagcacatttccgaaagtcgacacgctgacgtcctaagaacattattat					
Db	4758 AGGGGTTCGCGGACATTTCCCGGAAAGTGGCACCCTGACGCTTAAGAAACCATTTAT					
QY	15492 catgacattaaactataaaataggcgctatcacaggccctttcgtc					
Db	4818 CATGACATTAACTATAAAATAGCGTATCAGAGGCGCTTCGTC					
RESULT	5					
QY	074207 standard; CDNA; 4864 BP.					
Db	074207; 31-MAY-1995 (first entry)					
QY	074207; Expression vector Vlnneo.					
Db	DE Influenza virus; antigen; specific; immune response; nucleoprotein;					
QY	KW hemagglutinin; polymerase; matrix protein; non-structural protein;					
Db	KW human; vaccine; ds.					
QY	OS Synthetic.					
Db	PN WO9421797-A.					
QY	PD 29-SEP-1994.					
Db	PF 14-MAR-1994; U02751.					
QY	PR 18-MAR-1993; US-032383.					
Db	PR 08-JUL-1993; US-089985.					
QY	PA (MERI) MERCK & CO INC.					
Db	PA (VICA-) VICAL INC.					
QY	PI Donnelly JJ, Dwariki VJ, Liu MA, Montgomery DL, Parker SE;					
Db	PI Shiver JW, Ulmer JB;					
QY	PI WPI; 94-317017/39.					
Db	PT Polynucleotide vaccine comprising influenza virus genes - for					
QY	PT vaccination against more than one strain of influenza virus					
Db	PS Claim 6; Page 94-97; 17pp; English.					
QY	CC The sequences given in 074206-08 represent expression vectors which					
Db	CC were used for the expression of influenza virus genes. VJ contains					
QY	CC the contains the ampr gene and VJneo contains the kanR gene in the					
Db	CC same orientation. DNA constructs such as these, containing the					
QY	CC influenza virus genes are capable of inducing the expression of an					
Db	CC antigenic influenza virus gene product which induces a specific immune					
QY	CC response upon introduction of the DNA construct by cells which express					
Db	CC vivo and resultant uptake of the DNA construct into animal tissue in					
QY	CC the encoded influenza gene. The encoded influenza virus gene encodes					
Db	CC nucleoprotein, hemagglutinin, polymerase, matrix or non-structural					
QY	CC human influenza virus gene products. The virus gene is operably linked					
Db	CC to one or more control sequences for incorporation in a vaccine.					

Db	2838	GTAGGTGGTTTCGCTCCAAAGCTGGCGCTGTGTGCACGCAACCCCGGTTACGCCAGCGGTG	2897
Qy	13573	cgcttatccgggtaactatcgtcttgggtccaaacccgggtaagacacgacttatcgccact	13632
Db	2898	GGCCTTATCCGGTAACATATTCGTCTTGAGTCCAAACCCGGTAAGACACGACTTATCGCCACT	2957
Qy	13633	ggcagcagccactggtaacaggagattagcagagcgaggtatgtaggcgggtctacagagtt	13692
Db	2958	GGCAGCAGCCACTGGTAACAGGATTAGCAGACGGAGGTATGTAGCGGGTGTACAGAGTT	3017
Qy	13693	cttgaagtggtggtccaaactcaggtcactacactagaagaacagtatttggtactctcgctct	13752
Db	3018	CTTGAAGTGGTGCCCTAACATACGGGTACACTAAGAGGACAGATTTGTGTATCTCGGCTCT	3077
Qy	13753	gctgaagccagtttaccttcggaagagtggttagctcttgactccggtccgcaaaaacacac	13812
Db	3078	GCTGAAGCCAGTTACTCTCGGAAAAGAGTTGGTAGCTCTTGTATCCGGCCAAACAAACCAC	3137
Qy	13813	CGctggtagcgtggttttttggtttgaagcagcagattaccgcgcagaaaaaaggatc	13872
Db	3138	CGCTGTAGCGGTGGTTTTTGGTTTGCAGACGACGATTACGGCGAGAAAAAAGGATC	3197
Qy	13873	tcaagaagatcccttggactctttctagcgggtctgcagctccagtggaacgaaactcacg	13932
Db	3198	TCAAGAAGATCCTTTTGATCTTTTACGGGCTGTAGCGCTCAGGTGAACGAAACACTCAG	3257
Qy	13933	ttaagggtatttggatcagcagattatcaaaaaggattctcacctagatccctttaaatta	13992
Db	3258	TTAAGGGATTGGTCATGAGATTATCAAAAGGATCTTCACCTAGTACTCTTTAAATTA	3317
Qy	13993	aaaatgaagttttaaatcaatctaaagtatatatgatgaataactgctgcagagtaacca	14052
Db	3318	AAAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGCTGTGCAGTATCCA	3377
Qy	14053	atgcttaactcagtgagcaccatcttcagcgatctgtcttatttcgttccatccatagttgc	14112
Db	3378	ATGCTTAATCAGTGAAGCCTATCTACGCGATCTGTCTATTTCGTTCAATCATAGTTGC	3437
Qy	14113	ctgact-cggggggggggggcgtgaggtctgcctcgtgaagaaaggtgtgctgactcat	14171
Db	3438	CTGACTCCGGGGGGGGGGCGCTGAGGTCTGCCTCGTGAAGAGGTGTGCTGACTCAT	3497
Qy	14172	accaggcctgaatcgccccatcatccagccagaagtgaggagccagcgttgatgagag	14231
Db	3498	ACCAGGCTGAATCGCCCCATCATCCAGCCAGAAAGTGAGGAGCCACGGTTGATGAGAG	3557
Qy	14232	ctttgtgtagtgaggaccagttggtgatttgaacttttgcgttgcacaggaaacggtctg	14291
Db	3558	CTTTGTGTGAGTGGACCAAGTTGGTGATTGTGAACCTTTTGCTTCCACGGAGCGTCTG	3617
Qy	14292	cggtgcgggaagatcggtgatctgatccctcaactcagcaaaagttcgtatttataac	14351
Db	3618	CGTGTGCGGAGATGCGTGATCTGATCCTTCAACTCAGCAAAAAGTTCGATTATTTCAC	3677
Qy	14352	aaagccgcgtcccgctcaagtcagcgtaagtctctgcagtggttacaccaataaccaaa	14411
Db	3678	AAAGCGCGGTCCGCTCAAGTCAGCGTAATGCTCTGCCAGTGTGTACAAACAATAACCAA	3737
Qy	14412	tttgtattgaaaaaactcatcgacatcaataatgaactgaatttctcataccagatt	14471
Db	3738	TTCTGATTAGAAAACCTCATCGACATCAATGAAGAACTGCAATTTATTCATATCAGATT	3797
Qy	14472	atcaataccatattttgaaaaaagccgtttctgtcaatgaaggagaaactcaccaggca	14531
Db	3798	ATCAATACCATATTTTGA AAAAGCCGTTCTGTATGAGGAGAAATCTACCCAGGCA	3857
Qy	14532	gttccataggatgcagatcctggtatcggtgtcgattcccgacttcgctcaacatcaat	14591
Db	3858	GTTCCATAGGATGCAGATCCTGGTATCGGCTCGGATTCCGACTCGTCCCAACATCAAT	3917
Qy	14592	acaacctattaatttcccttcgctcaaaaataaggtttatcaagtggagaataccatgagt	14651
Db	3918	ACAACCTATTAAATTCCCTTCGTCAAAATTAAGTTTATCAAGTGAGAAATCAACATGAGT	3977

QY	14552	gaagactgaatccgggtgaaatggcaaaagcttatgcattttttccagactttgttcaac	14711
Db	3978	GAGCACTGAATCCGGGTGAAATGGCAAAAGCTTATGCAATTTCTTCCAGACTTGTCAAC	4037
QY	14712	agccagccattacgctctgcatacaaaatcactcgcatacaacaaacggttattcattcg	14771
Db	4038	AGCCAGCCATTACGCTGCTCATCAAAATCACTCGCATCAACCAACCGTTATTCATTCG	4097
QY	14772	tgattcgctgagcgagacgaatcacgcgcatcgctgtttaaagagacaattacaacagg	14831
Db	4098	TGATTCCGCTCGAGCGAGACGNAATACGCGATCGCTGTGTTAAAGGACAATACAAACAGG	4157
QY	14832	aatcgaatcaaccggcgagaaactgccagcgcatcaacaataatttcacctaact	14891
Db	4158	AATCGAATCAACCGCGCAGAAACACTGCCAGCGCATCAACAATATTTACCTGAATC	14911
QY	14892	aggatattcttaataactcgtgaatcgttttccgggagatcgagtcggtgagtaacca	14951
Db	4218	AGGATATTCTTAATACCTCGAATGCTGTGTTCCGGGGATCGCAGTGAGTAACCA	4277
QY	14952	tgcatacgaagtagcgataaaatcgttgatggtcggaagggcgataaaattccgtcag	15011
Db	4278	TGCATCATCAGAGTAGCGATAAAATGCTTGATGGTCGGAAGAGGCATAAATCCGTCAG	4337
QY	15012	ccagtttagtctgaccatctcaatctgaatacatcattggcaacgctacatttgcctgttt	15071
Db	4338	CCAGTTTAGTCTGACCATCTCATCTGTAAATCATTTGGCAACGCTACCTTTGCCATGTT	4397
QY	15072	cagaaacaactctggcgactcgggcttccatacaatcgatagatgtcgcaactgattg	15131
Db	4398	CAGAAACAATCTGGCGCATCGGGCTTCGCATACAATCGATAGATGTGCGACCTGATTG	4457
QY	15132	ccgcacattatcgcgaccattataccatatataaatcagcatccattgttggaaatttaa	15191
Db	4458	CCCGACATTATCCGGAGCCATTATACCACATATAAATCAGCATCCATGTTGGAATTAA	4517
QY	15192	tcggcgctcgagcaagacttcccgcttgaatacggctcaaacgcttccctgtattact	15251
Db	4518	TCGGCGCCTCGAGCAAGAGCTTCCGGTGAATATGGCTCATACACCCCTGTGATTACT	4577
QY	15252	gttatgtaagcagacagtttattgttcattgatgatataatttatctgtgcgaatga	15311
Db	4578	GTTTATGTAAGCAGACAGTTTTATTGTTCATGATGATATATTTTATCTGTGCAATGA	4637
QY	15312	acatacagattttgagacacacgtygctttccccccccccccccattattgaagcattta	15371
Db	4638	ACATCAGAGATTTCAGACACAACCTGGCTTCCCGCCCCCCCCCATTTATTAAGACATTA	4697
QY	15372	tcagggtattgtctcatgacggatataatttgatgtattagaaaaataaacaat	15431
Db	4698	TCAGGGTTATGTCTCATGCGGGATACATATTTGAATGTATTTAGAAAAATAACAAAT	4757
QY	15432	aggggttcgcgacatttccccgaaagtgccacctgacgctcagaagaccattattat	15491
Db	4758	AGGGGTTCGGGCATTTCCCGCAAAAGTCCCACTGAGCTTAGAAACCAATTATTAT	4817
QY	15492	catgacataacctataaaataggcgatcaacagggcccttcgtc	15538
Db	4818	CATGACATTACCTATAAAATAGGCGATTCACGAGGCCCTTTCGTC	4864

RESULT
V00677
6

ID V00677 standard; DNA; 5898 BP.

AC V00677;

08-JUN-1998 (first entry)

DNA plasmid VP2211 control

DNA plasmid VR2211 contains:

borrella; antigen; outer su
DNA vaccine; immunization; *Brucella*

DNA vaccine; immunisation; chimera; T cells

Chimeric - Borrelia burgdorferi

Chimeric - Homo sapiens.

Key	Location/Qu
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References

Sun Feb 13 13:44:46 2000

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FT primer_bind complement (2..19)
FT /*tag= a
FT /*note= "binding site of forward primer used to
FT amplify and insert OspB coding sequence"
FT primer_bind 835..852
FT /*tag= b
FT /*note= "binding site of reverse primer used to
FT amplify and insert OspB coding sequence"
PN W09747197-A1.
PD 18-DEC-1997.
PF 03-JUN-1997; U09439.
PR 14-JUN-1997; US-663998.
PA (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
PA (UYTE-) UNIV TEXAS HEALTH SCI CENT SAN ANTONIO.
PA (VICA-) VICAL INC.
PI Barbour AG, Carner KR, Huebner RC, Liang X, Luke CJ,
PI Norman JA.
DR WPI: 98-051938/05.
PT plasmid for expressing Borrelia antigen in eukaryotic cells - used
PT as vaccines to protect against Lyme disease and for production of
PT antigens, themselves used in vaccines
PS Example 1; Fig 4A-D; 80pp; English.
CC This is the nucleotide sequence of VR2211, a DNA plasmid suitable
CC for transfection of e.g. baby hamster kidney and human melanoma
CC cells. VR2211 contains DNA encoding the Borrelia burgdorferi
CC outer surface protein B (OspB). It was made by ligating: an OspB
CC fragment (see V00680) amplified from pTRH46 (see V00685-86); a
CC tissue plasminogen activator 5'-untranslated region/leader peptide
CC sequence amplified from pXCMVmtl (see V00678); and pSTI- and
CC XbaI-digested plasmid VR102. Plasmid DNA encoding at least one
CC Borrelia genospecies antigen is disclosed and claimed. The
CC Borrelia genospecies antigen is disclosed and claimed.
CC Genospecies may be B. burgdorferi, Borrelia garinii and/or
CC Borrelia afzelii. The antigen can be OspA and/or OspB and/or OspC.
CC The plasmid is used in vaccines to elicit a protective immune
CC response (both humoral and cellular) in hosts, human or animal,
CC susceptible to Lyme disease (claimed). It can also be used for the
CC production of a Borrelia antigen in vitro in eukaryotic cells
CC (claimed), and these antigens used as vaccines or immunogenic
CC compositions, or to produce monoclonal antibodies.
CC Sequence 5898 BP: 1643 A; 1402 C; 1380 G; 1473 T;
SQ
Query Match 18.9%; Score 2930; DB 1; Length 5898;
Best Local Similarity 99.5%; Pred. NO. 0;
Matches 2980; Conservative 0; Mismatches 10; Indels 4; Gaps 4;
Qy 12548 gatccagatctgctgtgcttctagtgccagccatctgttggccctcccgctgc 12607
Db 854 GATCCAGATCTGCTGTGCTTCTAGTTGCCAGCCATCIGTTGTTGCCCTCCCGGTGC 913
Qy 12608 ctctctgaccctggaagtgccactccactgctcttcttccataataaataaggaattg 12667
Db 914 CTTCCTTGACCTCGAAGTGGCCACTCCACTGCTCCITTCCTATAAATGAGGAATTG 973
Qy 12668 catcgattgtctgagtgagtgatctattcttggttggttggttggttggttggttggt 12727
Db 974 CATCGCAATGTCGATGAGTGTCTATTCTGTGGGGGGTGGGTGGGGTGGGTGGGTGGGT 1093
Qy 12728 aggggagatgggaagacacatagcagcagcagcagcagcagcagcagcagcagcagcagc 12787
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Qy 12848 ttctctgaacacacctgtlccacgcccctggttctttagttccagcccccaatcataggac 12907
Db 1154 TTCTCTGTGAACACCTGTGTCACGCCCCCTGTTCTTCTAGTTCCAGCCCCCACTCATAGAC 1213
Qy 12908 actcatagctcaggagggtcccgcttcaatcccaaccctaaagtacttgagcggtct 12967
Db 1214 ACTCATAGCTCAGGAGGCTCCCGCTTCATCCACCCCGCTAATGACTTGGAGCGGTCT 1273

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Copied from 09549937 on 04/17/2006

RESULT 7

CC response (both humoral and cellular) in hosts, human or animal, susceptible to Lyme disease (claimed). It can also be used for the production of a Borrelia antigen in vitro in eukaryotic cells (claimed), and these antigens used as vaccines or immunogenic compositions, or to produce monoclonal antibodies.

CC Sequence 5843 BP; 1611 A; 1390 C; 1385 G; 1457 T;

Query Match	18.8%;	Score 2919.2;	DB 1;	Length 5843;
Best Local Similarity	99.9%;	Pred. No. 0;		
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QY 12608 ctctcgtgacctggaaggtgccaactccactgctcttcttaataaattgaggaattg 12667				
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QY 12668 catgcattgtcagtagtgctattctattct-ggggggtgggtggggcaggacgc 12726				
Db 1110 CATCCATGTCTGAGTAGGTGCTATCTATCTGCGGGGTGGGGCAGCACAGC 1169				
QY 12727 aaggggggagattgggaagacaatagcagcatctgggatcggtgggtctctatgggt 12786				
Db 1170 AAGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTCTATGGGT 1229				
QY 12787 acccaggtgctaagaattgaccgggttctctcctgggcagaaagagcagcatccc 12846				
Db 1230 ACCGAGTGCTGAAGANTGACCGGTCTCTCTGGGCGAGAAAGAGCAGCATCCC 1289				
QY 12847 ctctctgtgacacacctgtccagccccctgttcttagttccagcccactcatgga 12906				
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QY 12907 cactatagctcaggggctcgcttcaatccacccgcgttaagtacttggagcggtc 12966				
Db 1350 CACTCATAGCTAGGAGGCTCGGCTTCAATCCACCGCTTAAAGTAGTACTTGGAGCGGTC 1409				
QY 12967 tctccctccctctatcagcccccaaaaccacaaactagctcccaaggtgggaagaaataa 13026				
Db 1410 TCTCCCTCCTCATCAGCCCAACCAACCAACCTAGCTTCCAGAGTGGGAGAAATTA 1469				
QY 13027 agaagatagctattaaagtgcagagggagagaaatgctcccaacatgtgaggaagtaa 13086				
Db 1470 AGCAAGATAGCTATTAAGTGCAGAGGAGAGAAATGCTCCACATGTGAGGAAGTAA 1529				
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QY 13327 tcgagcgtcaagtgcagaggtggcgaaccgacagagactataagataccagcggttcc 13386				
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Db 1830 CCCTGGAAGCTCCCTCGCTGCT 1889				
QY 13447 cgcctttctccctcgggaagcggtggtcttcttctatagatcagctcagctgtaggtatctcag 13506				

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QY 13987 aaattaaaaatgaagtttttaaatcaatcaatgaatataatgaagtaaatgtgtgtgacag 14046				
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Db 3807 CATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTTGAATGATTTTAGAAAAATRA 3866
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Db 3927 TTATTATCATGACATTAACCTATAAAATAGGCGTATCAGGCGCTTTCCTC 3980

RESULT 8
ID V33473
AC V33473
DT 10-DEC-1998 (first entry)
DE South African Arbovirus strain No. 86 cDNA sequence.

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KW Bone marrow cell; alphavirus: South African Arbovirus strain No. 86;
KW S.A.AR86; reverse transcriptase-PCR; nsP1; nsP2; nsP3; nsP4; capsid;
KW E3; E2; 6K; E1; growth hormone; growth factor; interleukin; cytokine;
KW chemokine; enzyme; ribozyme; antisense oligonucleotide; ss.
OS South african arbovirus
FH Key 1
FT 5'UTR Location/Qualifiers
FT 1..59
FT /*tag= a
FT CDS 60..7662
FT /*tag= b
FT /*product= "Non-structural polyprotein"
FT CDS 7608..11345
FT /*tag= c
FT /*product= "Structural polyprotein"
FT 3'UTR 11346..11663
FT /*tag= d
PN W09836779-A2.
PD 27-AUG-1998.
PR 18-FEB-1998; U02945.
PR 19-FEB-1997; US-801263.
PA (UYN-) UNIV NORTH CAROLINA.
PI Davis NL, Johnston RE, Simpson DA;
DR WPI: 98-495361/42.
DR P-PSDB; W70460; W70461, W70466, W70467, W70468, W70469, W70470;
DR P-PSDB; W70471, W70472.
DR Expression of heterologous RNA in bone marrow cells - using a
PT recombinant alphavirus comprising a promoter operable in bone marrow
PT cells operably associated with heterologous RNA.
PS Example 2: Fig 1A-1C; 88pp; English.
CC The invention provides a method for introducing and expressing
CC heterologous RNA in bone marrow cells using alphavirus vectors.
CC The South African Arbovirus strain No. 86 (S.A.AR86) is an
CC alphavirus whose cDNA sequence was determined from unclooned reverse
CC transcriptase-PCR reaction fragments amplified from the virion RNA.
CC The S.A.AR86 cDNA encodes nonstructural and structural polypeptides.
CC The nonstructural polypeptide is, presumably, post-translationally
CC modified into four different protein products, namely nsP1 (W70460),
CC nsP2 (W70461), nsP3 (W70466), nsP4 (W70467) proteins. The structural
CC polypeptide is, presumably, post-translationally modified into five
CC different protein products, namely capsid (W70468), E3 (W70469),
CC E2 (W70470), 6K (W70471), E1 (W70472) proteins. The S.A.AR86 cDNA
CC used in the method of the invention. The inventors claim the
CC transformed bone marrow cells are useful for expressing a protein or
CC peptide suitable for protecting the subject against a disease such as
CC a microbial, bacterial, protozoal, parasitic or viral disease. The
CC transformed bone marrow cells are also claimed to be useful for
CC expressing proteins and peptides such as hormones, growth hormones,
CC growth factors, interleukins, cytokines, chemokines, enzymes, ribozymes
CC or antisense oligonucleotides.
SQ Sequence 11663 BP; 3291 A; 3105 C; 2907 G; 2360 T;

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Query Match 14.6%; Score 2272.8; DB 1; Length 11663;
Best Local Similarity 58.4%; Pred. No. 2.9e-263;
Matches 4385; Conservative 0; Mismatches 2892; Indels 237; Gaps 14;

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Qy 2704 gtcgttcgaggtgagtcattcaggtcacacaaatgacctgcaaatgagcagcatt 2763
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Qy 2764 ttccgacctggctaccaaattgatcagcagcagcagcagcagcagcagcagcagcagc 2823
Db 194 TTGCGATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCTTACACAGCGAGATTGGA 253
Qy 2824 tatcggcagtcgcttccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2883
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4555 ccatattcgcttcacgagccgtcgctgaacacgcagcagcagcagcagcagcagcagcagc 4614
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3424 attccacctgaagggttaacaaatcctttactgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3483
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3484 aggtgactgttgaagaaataactatgtgcccgcgtgctgacgtataaaaggttaggtga 3543
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3544 cgcgtgacgtatcacgcgagaggtccttagtgtgaagacacacagacactgtcaaggg 3603
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3604 agaaagagttcttccctgtatgcacctcgtccctcagcagcagcagcagcagcagcagcag 3663
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3724 tcagsggagttgtgacggaagaaacacagcagcagcagcagcagcagcagcagcagcagc 3783
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3784 gcttcagattgtgctcgcatttagcaggtggcgagagagagagagagagagagagagagag 3843
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3904 taaacagagagatgacacacatataaagaacacacacacacacacacacacacacacacac 3963
1331 TCGCACTAAGAAAGTGCATCTGTTATCGCCCACTCGAAGCAGACCATCGTAAAGT 1390
3964 gcttcagaggttaactcgt 4023

QY	5095	cgagttcttcaatatgatcgagcttaagggaacttcaaccac-----aacatctg	5145
DB	2531	CGGATTCCTTCAACATGATGCAACTAAAGGTACATTTCAACCACTTGAAGAACATATG	2590
QY	5146	cactgaagcatgtctataaagatatatccagacgtctgcacgcgtccagtcacggccatcgt	5205
DB	2591	TACCACAGACATCTACAAGTTATCTCCCGACGCTGCACACAGCCAGTCACGGCTATGCT	2650
QY	5206	gtctacgttgctactcaggaagcgaagatgctgcacgacacacccgtgcacaaacccataat	5265
DB	2651	ATCGACACTGCTACGATACGATGAAAAATGAACACCAACCCGCTCGAAGAACATCGA	2710
QY	5266	catagacaccacagacagaccagaagcccaagccagagacatcgtttaacatgcttcg	5325
DB	2711	AATCAGACATTCACGGGCCACGAAGCCGAAGCAGCGAGACATCATCTGACATGTTTCGG	2770
QY	5326	aggctgggcaagcagctgcagttggactaccgtgcagacgaagaatcatgacacgacgc	5385
DB	2771	CGGCTGGGTTAAGCAACTGCAAAATGACATATCCCGGACATGAGTAATGACACGCCGCG	2830
QY	5386	actctcagggctcaccgcgaaggggtatacgcogtaaggcagaagtgtaataaaatcc	5445
DB	2831	CTCAGAGGGCTTACCAGAAAGAGTAGTATATCGCTCGCGCAAAAAGTCAATGAACCC	2890
QY	5446	cttgatgccctgcgtcgagacagtgaaagtactctacgcgcactgcaggtataggct	5505
DB	2891	GCTGTAGCCGATCACAATCAGACGATGTACAGCTGTTGCTCACCAGCCTGAGGACAGCT	2950
QY	5506	ggctggaacacgtgcgcggcggaacctggattaaaggtctctcaaacattccacagg	5565
DB	2951	AGTATGAAATTTTACAGGGCGACCATATGATTAAGCAGCTCACAATACCTTAAGG	3010
QY	5566	taactttacggccacattggaagatgccaagaagaacacacaaataatgaaggtgat	5625
DB	3011	AAATTTTCAGGCCACCATCGAGGACTGGGAAGCTGAACACAGGGAATAATTTGTGCGAT	3070
QY	5626	tgaagacccgctgcgcgtgtggacgogtttcagaacaaagcgacgtgtgttggggcga	5685
DB	3071	AAACAGTCCGCTCCCGTACCATACTCGTTTCAGCTGCAAGACTAACGTTGCTGGGGAA	3130
QY	5686	aagcctgggtgcctctgggacactgcggaatacagatgcagcagagggagtgagcac	5745
DB	3131	AGCAGCTGGAACGACTACTGCGCCAGCGCGGTATCTGACTTACCGGTTCCAGTGGAGCGA	3190
QY	5746	caatactcagcatttaaggaggacagagcttactctccagtggtggccttgaataaat	5805
DB	3191	GCTGTTCACAGTTTCGGATGACAAACACACTCGGCCATCTACGCTTTAGACGTAAAT	3250
QY	5806	tgcaccagtaactatgagttgacctggacagtgcctgtttctgccccgaagtgct	5865
DB	3251	TTGCATTAAGTTTTTCGGCATGCACTTGACACGGGGGTGTTTTCCAAACAGAGCATCCC	3310
QY	5866	ctgtattacagagaaac-----cacitggataacagacactgg	5904
DB	3311	GTTAACGTAACCATCTCCGACTCAGCGGCCAGTAGCTCATTTGGACACACGCCACGG	3370
QY	5905	tgaagagatgatgtgattcaatccgcaacagctccaggtcggagctgacatacctt	5964
DB	3371	AACACGCAAGTATGGGTACGATCAGCCCGTTGCCCGCAACTCTCCCTCAGCCTTAGTCCC	3430
QY	5965	cctgaaggggcagtggtcattcagggcgaagcaggcagttatcgagaagaataatccaac	6024
DB	3431	GTTCAGCTAGCTGGG---AAAGGCACACAGCTTGATTTCGACNAGGGCGAAGCTAGAGT	3487
QY	6025	gctttctgtctggagcaatgaattccatctcaacgcgcaggtgcgcacgcgcttggtg	6084
DB	3488	TATCTCTGCACACGATTAATTGTTCCCTAGTGAACCGCAATCTCCCTCAGCCTTAGTCCC	3547
QY	6085	tgaatacaagcgytttaaaggcagtagggtttgagtgctggttcaataaagtaagaggta	6144
DB	3548	CGAGCACAAAGGAACAAACCCGGCCCGTTCGAAAAATCTTGAGCCAGTTCAACACACA	3607

QY	6145	ccacgtcctcgtgtagtgagtagaacacctggctttgctcctcgaacgagggtagtacttgggtt	6204
Db	3608	CTCGTACTTGTGATCTCAGAGAAAAAATTGAAGCTCCCCACAACAGAATCGAATGAT	3667
QY	6205	gtacccgctgaatgttcaacagcgccgataggtgtctacgcacctaagttttaggactgcggc	6264
Db	3668	CGCCCCGATTGGCATAGCCGGCCGACATAGAAGAACTACAACCTGGCTTTCGGGTTTCCGCC	3727
QY	6265	tgaocgcggcaggttctcgacttggctcttttgaacattcacacggaattcagaataccaca	6324
Db	3728	GCAGGC---ACGGTACGACCTGGTGTTCATCAATATGGAACATAATACAGAAACATCA	3784
QY	6325	ctaccagcagtgctgcacacgcacctaagctgcagatgcttgggggagatgcgctacg	6384
Db	3785	CTTTCACAGTGGGAAGACACCGCGGACCTTGAAAACCCCTTCGCGTTCGGCCCTGAA	3844
QY	6385	actgctaaacccggcgga----tttggatgagagcttacgatacgcgcgtataaaatcag	6441
Db	3845	CTGCCTTAACCCCGGAGGCACCTCGTGGTGAAGTCCACGGTTACGCGGACCCGCAATAG	3904
QY	6442	cgaagcgtgtttcctccttaagcagaagaagtctcgtcgaagagtgttgcgcccgga	6501
Db	3905	TGAGGACGTAGTACCGCTCTTGCCAGAAAAATTGTTCAGAGTGTCTGCAGCGAGCCAGA	3964
QY	6502	tttgttcaccagcaatacagaagtgtcttctgtcttctccaactttgacacggaaagag	6561
Db	3965	GTGCGTCTCAAGCAATACAGAAATGTACTCTGATTTTCGGACAACTAGACAAACGCCAC	4024
QY	6562	accctctacgtctacacagatgaatacaagctgagtgccgtgtatccgggagaagccat	6621
Db	4025	ACGACAAATTACCCCGCATCATTTTGAATTGTGTATTTCTCGGTGACGAGGTACAG	4084
QY	6622	gcacacggccgggtgtgcacatcctacagagtttaagagagacagacatagccacgtcac	6681
Db	4085	AGACGGAGTTGGAGCCGACCGTCTACCGTACTTAAAGGAGGAACATTCGTGATTGTCA	4144
QY	6682	agaagcggctgtttaacgcagctaaacgcgcgttaacgttggaactgtagggaatggcgtatgcag	6741
Db	4145	AGAGAAAGCATTTGTCAATGACGCCAATTCACCTGGGCAGACCAGGAGAGGAGTCTGCCG	4204
QY	6742	ggccgtggcgaagaaatggccgtcagcctttaaggagagcagaacaaccagtgggcaaat	6801
Db	4205	TGCCATCTATAAACGTTGGCCGAAACAGTTTACCGAATTCAGCCACAGACAGATACCGC	4264
QY	6802	taaaacagtcagtgtgcgctcgtaccocgtctatccacgctgtagcgcttaattctctcgc	6861
Db	4265	AAAACTGACTGTGTGCCAAGAAAGAAAGTATCCACGCGGTGCGCCTGATTTCCGGA	4324
QY	6862	cacgactgaagcgggaagggaaocgcgaattggccctgtctaccggggaagtggccgcga	6921
Db	4325	ACACCCAGAGGCAGAGCCCTGAAATTGCTGCAAAACGCCCTACCATGCAAGTGGCAGACTT	4384
QY	6922	agtaaacagactgtcactgagcagcgtgaccatcccgctgtctgcacagggcgtttcag	6981
Db	4385	AGTAAATGAACATAATATCAAGTCTGTCCCATCCCACTGCTATCTACAGGCATTTAGC	7044
QY	6982	cggcggaagagataggctgcagaatccctcaacgctgtctgcacagggcgtttcag	7041
Db	4445	AGCCGAAAAAGACCCCTTGAGGTATCACTTAACCTTGCAACACCCGGCTPAGACAGAAC	4504
QY	7042	ggaagctgagtgaccatctactgcagagacaaaagtgtggagagaataatccagggaagc	7101
Db	4505	TGATCGGACGTTAACCATCTACTTGCCTGGATAAGAAAGTGAAGGAAGAAAGATTCGACGCGT	4564
QY	7102	cattgacatgagcagcgtcgt---ggattgctcaatgatcagctggagtgcaccaga	7158
Db	4565	GCTCAACTTAAGGAGTCTGTAACCTGAGCTGAAGGATGAGGATATGAGATTCACGACGA	4624
QY	7159	cttgttgagatgaaccgggacagcagctggtggttcgtaaaggctcacagttaccactga	7218
Db	4625	GTTAGTATGGATTCATCCGGACAGTTGCCTTGAAGGGAAGAAGGGATTCACTACTACAAA	4684
QY	7219	cggtgcgtgtactcgtactttggaagtacgaataatcaacaggctgttatgatggc	7278

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Db 5765 GCAAAAGAGTCGTTCTGACAGAACCCAGCTTACAGAACCCGACCTTTGGAGCGCAATGTTCT 5824
QY 8179 ggagaaatgtatccgcgaataatggaatactgagggagagctgtgtgctgtaaaat 8238
Db 5825 GGAAGAATCTACGCCCGCGTCTGACACAGTCGAAGAGGAGCAAGCTCAAACTCAGGTA 5884
QY 8239 gcagatcacccatcgagaggttaataagagtgatgataccagctctcgaagtgagaaat 8298
Db 5885 CCAGATATCCCGACGAGCCCAACAAAGCAGTACCACTGCTCGAAAGAGTGAAGAACCA 5944
QY 8299 gaaagccacggtggtgagaggtgagaggtgagaggtgagaggtgagaggtgagaggt 8358
Db 5945 GAAAGCCATACCACTGAGGAGTCTTTCAGGCTTACGACTGATA---ACTCTGCCAC 6001
QY 8359 aggcgcgcataacacacatcggtggtggtggtggtggtggtggtggtggtggtggtggt 8418
Db 6002 AGATCAGCCAGAGTCTTAAAGATCAGTACCCGAAACCATCTATTCAGCAGTATACC 6061
QY 8419 cgaagattctcaagcccgatgtagcaatcgaggtgcaacgaatacctatccagaa 8478
Db 6062 AGCGAATCTCTGACCCAAAGTTTGTGTAGTCTTGTAACTATCTGATGAGAA 6121
QY 8479 ttacccacagtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 8538
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QY 8539 tgacgggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 8598
Db 6182 AGACGGGAGTCTGCTTGTAGTACTGCAACTTTTTCGCCGCGCAAGCTTAGAAGTTA 6241
QY 8599 cccgaacatcgatcgatccaccagcgatgtagcagtggtggtggtggtggtggtggtggt 8658
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QY 8659 gaacacatcacagagagtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 8718
Db 6302 GAACAGTTTGAAGAGTCTGCTTATTCGCCGAGTAAAGAACTGCAACAGTACACAAAT 6361
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Db 6362 CGTGAACCTGCGCACTGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGT 6421
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Db 6542 GCATAATTTGTTCCATTTGCAAGAGTCTTATGATAGTCTGATGATGATGATGATGAT 6601
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Db 6662 ACAAGCCGAGAACCCCTTGGCGAGTCTTACCTATGCGGATCCACCGGAGTATGCGG 6721
QY 9079 gagactaatgctggtgag 9138
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QY 9139 ctttacgcgatacgcctctcactccaccagagagagagagagagagagagagagagagag 9198
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QY 9199 tgcatactcgaag 9258
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3004	QY	ggctacgcgcagcgcgtgaattctctctacatttgcctgcatacacagcgtcaacgtctcgtac	3063
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3064	QY	ggcagcgaagtggccgtataccaggaacgtgtatcgtgtacatgcacaaacatgcgtata	3123
494	DB	CGGTGCCGAGTACTCGGTATCGACGACGCTGA---CATCAACGCTCCGGAACTATTATTA	550
3124	QY	caatacggcgatgaagaaggtgcagaacgcgttatctggattgggtttgacacacccccgtt	3183
551	DB	CCACAGGCTATGAAGGGCTGCGGACCCCTGTATGATTGGCTTCGACACACCCAGT	610
3184	QY	tatgtttgacgcgtacgagcgcgctatccaacctacgcacaaactggccgcagcagca	3243
611	DB	CATGTTCTCGGCTATGGCAGTTCCGTACCTGTCATACACACCACTGGCGCGACGAAAA	670
3244	QY	ggtgtttacagccaggaacatagactgtgtgcagcatccttgactgaggggaagactcgg	3303
671	DB	AGTCCTTGAAGCGCGTAACATCGGACTCTGCACACAAAGCTGAGTGAAGGCAGGACAG	730
3304	QY	caaaactgtccattctccgcaagaagcaaatgaaaccttgcgcacacgtcatgtctcgtt	3363
731	DB	AAAGTTGTCGATATGAGGAAGAGATTGAAGCCCGGTACCGGTTTATTTCTCCGT	790
3364	QY	agatcacattgtacactgagcagcagaagactactgagagctgtgcacttacccctcgt	3423
791	DB	TGGATCGACACTTTTACCCACAAACACAGCCAGCTTGACAGCTGGCACTTCCATCGGT	850
3424	QY	attcacctgaagaggttaaaccaatccttaccttagtgcgtatccatcgtatcatgtga	3483
851	DB	GTTCCACTTGAAAGGAAGCAGTCGTACACTTGCCTGTGTATACAGTGTGAGCTGCGA	910
3484	QY	aggttaacgtagttaagaaaaatcactatgtccccgcgctgtacgttaaacgctagggt	3543
911	DB	AGGCTACGTAGTGAAGAAAATTCACCATAGTCCCGGATCACGGGAGAACCGTGGGATA	970
3544	QY	cgccgtgcgtatcacgcggaggattcctagtgtgcaagaccacagacactgtcaagg	3603
971	DB	CGCGGTTACAAACAATACGAGGGGCTTCTTGCTATGCAAAAGTTACCGATACGTAAAGG	1030
3604	QY	agaaagctctcattccctgtatgcactacgtccctcaaccatctgtatcaaatgac	3663
1031	DB	AGAACGGGTATCGTTCCCGGTGTGCACGTATATCCGGCCACCATATCGCATCAGATGAC	1090
3664	QY	tggcatactagcagccgcgtcacaccggagagcagcagaagttgttagtggagttgaa	3723
1091	DB	CGGCATATGGCCACGGATATCTCACTGACGATGCACAAAAAGTTCTTGGTGGGCTCAA	1150
3724	QY	tcagaggatagtgtgaacgggaagaacacagcagaacactaacacgatgaagaactatct	3783
1151	DB	CCAGCGAATTCGTATTAAACGGTTAAGCTAACAGGAACACCAATACCATGCAAAATTACCT	1210
3784	QY	gcttcgattgtggccgtcgcatcttagcaagtggcgagggaatacaaggcagaccttga	3843
1211	DB	TCTGCCAATCATGTGCACAAAGGTTTCAGCAAAATGGGCCAAGGAGCGCAAGAGATCTTGA	1270
3844	QY	tgataaaaacctctgggtgtccgagagaggtctacttactctactctgtgtggcatt	3903
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3904	QY	taaaacgaggaagatgcacaccatgtacaagaacacagacacccacagacaatagtgaagt	3963
1331	DB	TCCGACTAAGAAAGTGCACCTGTTCTATCGCCACCTTGAACGCAGACCATCGTAAAAAGT	1390
3964	QY	gccttcagatgttaactcgtctcgtatcccgagcctatggtctacagccctgcgaatccc	4023
1391	DB	CCACAGCCTCTTTTAGCGCTTTCGCCATGTATCCGTATGACTTACCTCTTGGCCCATGTC	1450
4024	QY	agtcagatcacgcattaagatgcttttggccaagaagacccaagcgagagttaatacctgt	4083
1451	DB	GCTCAGGCAGAGATGAATGGCATTTACAACCAAAAGAGGAGGAAAAAATGTCGCAAGT	1510
4084	QY	tctgcagcgt-----cgtcagccagggatgctgaacaagaggagagagaggttggaa	4137

Db	1511	CCGGAGGAATTAGTTATGAGGCGCAAGCTGCTTTTCAGGATGCTCTCAGGAGGAATCCAG	1570
QY	4138	ggccgagctgactagagaagccttaccacctcgtccc---catcgccgcgcgcgagac	4194
Db	1571	AGCGGAGAAGCTCCCGAGAAGCACTCCCAACCAATTAGTGCACACAAGGTATCGAGGCAGC	1630
QY	4195	gggagtcgtcgacgtcgacgttgaagaactagatcacgcaggtgcaggggtcgtgga	4254
Db	1631	TGCGGAAGTTGCTGCGAAGTGCAGGGCTCCAGCGCGACACCAGGAGCAGCACTCGTGCGA	1690
QY	4255	aacacctgcagcgcgcttgaagagtcacgcacagccgcaacgacgtactactaggaaatta	4314
Db	1691	AACCCCGCGCGGTATGTAAAGGATAATACCTCAAGCAATGACCGTATGATCGGACAGTA	1750
QY	4315	cgLagttctgtcccccgcagaccgctcacaagagctccaaagttyggcccccgtcacccctct	4374
Db	1751	TATCGTTGTCCTCCGATCTCTGTGCTGAAGAAGCTAACTTCGACACGACACACCCGCT	1810
QY	4375	agcagagcaggtgaaataataaacataaacgggagccgcgcgttaaccaggttcacgg	4434
Db	1811	AGCAGACACAGGTTAAAGATCAATACCGCACTCCGGAAGATCAGGAAGGTATGCAGTCGAACC	1870
QY	4435	atatgcgcgagggctccactaccatgtggatcggccattcccggttcctctgagdtccaagc	4494
Db	1871	ATACGACGCTAAAGTACTGATGCCAGGGAAGCTGCGGTACCATGTCGCAAGATTCCTAGC	1930
QY	4495	tttagcgaagcgccactatggtgtacacgaaggaggttcgtcaacaggaaactata	4554
Db	1931	ACTGAGTGTAGAGCGCCACGCTGTGTGTACACGAAGAAGAGATTTGTGAACCGCAAGCTGA	1990
QY	4555	ccattatgcggttcacgcgacgctgcgtgaacacacgcagaggagaaactacgagaaagtcag	4614
Db	1991	CCATATTGCCATGCACGGTCCCGCTAAAGATACAGAAGAGGAGCAGTACAAAGTTACAAA	2050
QY	4615	agctgaagaactgcagccgcagtagctgttcgacgtagataaaaaatgctgcgtccaagc	4674
Db	2051	ggcagagctccgaacaaacagagtagtgcgtgttgacctgcgcacagaagcgcgttaagaa	2110
QY	4675	agagaaagctcggggttgggtgtgtggtagagctaaccaaccccccggttcacatgaatt	4734
Db	2111	GGAGAAGCCCTCAGGACTGTGTCTTGGGAGAACTGACCAACCCGCCCTATCACGAACT	2170
QY	4735	cgcctcagaaggctgaagatcagccgctcgccaccataaagactacagtagtaggagt	4794
Db	2171	AGCTCTTGAGGACGTGAAGACTGACCCCGCGTCCCGTACAAAGTTGAAACAATAGGAGT	2230
QY	4795	ctttgggggttcgggatacaggcaagtcgtctattattaagagcctctgaccacaacga	4854
Db	2231	GATAGCACACCAGATCGGCAAGTCAAGTATCATCAAGTCAACTGTCACGGCACGTGA	2290
QY	4855	tctggtcaaccagcgcgaagaagaaactgcaggaataagttaacgacgtgaagaagca	4914
Db	2291	TCTGTGTACCGGGAAGAAAGAAACTGCCGGAATTGAGGCCGACGTCGTACGGCT	2350
QY	4915	cgcgggaagggaagtaggggaataacagtgactccatcctcgtctaaacggggtcgtcgcg	4974
Db	2351	GAGGGCATGCAGATCACGTCGAAGACAGTGGATTTCGTTATGTCTCAACGGATGCCACAA	2410
QY	4975	tgcgtggacatactctatgtgacgagccttcgcttgcaattccggtactctcgtctggc	5034
Db	2411	AGCCGTAGAAAGTGCTGTATGTTGACGAACGTTCCGGTGCCACGAGGACACTACTTGC	2470
QY	5035	cctaattgctctgtttaaacctcggagcaaatggtgttatcgagagaccacaacatg	5094
Db	2471	CTTGATTGCAATCGTCAGACCCCGTAAAGAGGTAGTACTATCGGAGACCCCTAAGCAATG	2530
QY	5095	cggattctcaatatgatcagcttaagtgaaacttcaaccac-----aacatctg	5145
Db	2531	CGGATCTTCAACATGATGCACTAAAGGTACATTTCAACCACCTGTAAAGAGACATATG	2590
QY	5146	cactgaagtagtgcataaagtgataccagacgtttgcacgctccagtcacgcccacgt	5205

D	b	2591	TACCAGACATTC	TACAAAGTTTATCTCCGACGCTTG	CACACAGCCAGTCACGGCTATTGT	26550		
Q	y	5206	gtctacgttg	cactacagagcg	caagatgcgcagaccacccg	tcacacaaaccccaaat	5265	
D	b	2651	ATCGACACTG	CAATTACCATG	GAATAAATGAAACCAACCAACCCG	TGCAGGAAGAACATCGA	2710	
Q	y	5266	catagacaccac	agagacagacc	aagcccaagccagagacacatcgt	gttaacatgccttcg	5325	
D	b	2711	AATCGAATTA	CACAGGGCCACG	AAGCCGAAGCAGGGACATCATCT	GTGACATGTTTCCG	2770	
Q	y	5326	aggtctggg	cgaagcagctgc	gttgactacgttgacacgaagtc	atgcacagcagcagc	5385	
D	b	2771	CGGTGGTTT	AAGCACTGC	AATGACTATCCCGGACATGAGT	ATATACAGCCGCGC	2830	
Q	y	5386	atctcaaggc	ctcaccgcgaagggg	tatacgcgttaagcgagaggtgaat	gaaatcc	5445	
D	b	2831	CTCAAGGGCT	AACAGAAAAAG	AGTAGTATCGCTCGCGCAAAAGTCA	ATGTAAGAACCC	2890	
Q	y	5446	cttgtatgc	ccctgcgtgagcagctgaat	gtactgtacgcgcactgagataggct		5505	
D	b	2891	GCTGTACG	GGATCATATCAG	ACTGTGAACGTGTGCTCACCGCACT	TGAGACAGCT	2950	
Q	y	5506	ggtgtgga	aaacgcgtggcg	cgatccctggattaaagttcctatacaac	tattccacagg	5565	
D	b	2951	AGTATGGA	AAACTTTAC	AGGGCGACCCATGATTAAC	CAGCTCACTACCTACCTAAAGG	3010	
Q	y	5566	taactttac	gcgcacatgga	gaatggaagaaacacgcacacaaataat	gaaggtgat	5625	
D	b	3011	AAATTTT	AGGCCACCATC	GTAGGACTGGGAAGCTGAACAAGGAA	TAATTTGTCGCAT	3070	
Q	y	5626	tgaagac	cggctgcgcgtt	ggagcgttccagaacagcgaacgtgtgt	gtggcgaa	5685	
D	b	3071	AAACAGT	CCCGTCCCGT	CCCAATACGTTTACGCTGCA	AGACTACGTTGCTGGCGAA	3130	
Q	y	5686	aagcctgg	tgccttccttg	gcacatgcggaaatcagatgacagcag	aggagtgagcac	5745	
D	b	3131	AGCACTG	GAACCGAT	TGCGGATGCAAAACACACTCG	GCCATCTACGCTTAGACGTAT	3250	
Q	y	5746	cataattac	agcattaa	aggagagacagcttactctcagtggt	ggcctggaatgaaat	5805	
D	b	3191	GCTGTTC	CCACAGTTT	CGGATGCAAAACACACTCG	GCCATCTACGCTTAGACGTAT	3250	
Q	y	5806	ttgcacca	agtactatg	aggttaccctgcacagtcgctgtttct	gtcccccgaagtgct	5865	
D	b	3251	TTGCATT	AAGTTTTT	TCGGCATGACTTGACAAGCGG	GTGTTTTCCAAACAGAGCATCC	3310	
Q	y	5866	cctgtattac	agagaaac	-----cactggataacagac	ctgg	5904	
D	b	3311	GTAACTAG	TCACTCTCCG	CACTACGAGGCCAGTACTCTAT	TGGCAACACAGCCAGG	3370	
Q	y	5905	tgaagga	tgtatg	gattcaatgcgcacagctgcgaagct	ggaagctagacatacct	5964	
D	b	3371	AACAGC	CAATGTGGT	ATGATCAGTCAGCGGTTCGCGCGA	ACTCTCCGTAGATTCCCGT	3430	
Q	y	5965	cctgaagg	ggcagtggt	cacacgcgcagcttatcgagaa	gaaataccaac	6024	
D	b	3431	GTTCAC	AGTACTG	CGG- ---AAAGGCACACAGCTTG	ATTGCAACGGCAGAACCTAGAGT	3487	
Q	y	6025	gcttctgt	ctggaacat	gttaattcctataccgcagagctgcgc	cagccctggtggc	6084	
D	b	3488	TATCTCT	GCACAGAT	TAATTGGTCCCAGTGAACCGGA	ATCTCCCTACGCTTAGTCC	3547	
Q	y	6085	tgaataca	agcgtgttaa	aggcagtagggttgagtggttc	caataaagtaagaggta	6144	
D	b	3548	CGAGCA	CAGGAGAA	CAACCGCGCGGTGCGAAAAAT	CTTGAGCCAGTTCAAAACCA	3607	
Q	y	6145	ccacgt	ctctgc	gtggagtgagtaacac	ctggcttcgtcgcagcgaggttcact	6204	
D	b	3608	CTCCGT	ACTGTG	ATCTCAGAGAAAAAAT	TGAAGTCTCCCAAGAGAAATCG	ATGGAT	3667
Q	y	6205	gtcacgc	ctgtaat	gtccagcgcgcagtaggt	gtactacgacataagtttag	actgcccgc	6264
D	b	3668	CGCCCG	CGATTG	CAATAGCCGCGCAGATAGAA	CTACAACCTTGGCTTTCCGGT	TTCCGCC	3727

Qy	6365	tgacgcggcaggttcgacttgctcttggaaacattcacaggaattcagaaatcacca	6324
Db	3728	GCAGGC---ACGGTCAGACCTGCTGTTTCATCATATTGGAACATAAATACAGAAACCATCA	3784
Qy	6325	ctaccagcagtgctcgaccagccatgaagtgcagatgcttgggggagatgcgtacg	6384
Db	3785	CTTTCAACAGTGGGAAGACACGCGCGACCTTGAAACCCCTTCGCGTTCGCGCCCTGAA	3844
Qy	6385	actgctaaacccgggg---catcttgatgagagcttacgatacgcgataaaatcag	6441
Db	3845	CTCGCTTAACCCCGGAGGACCCCTCGTGTGAAGTCCTACGCTTACGCGGACCGCAATAG	3904
Qy	6442	cgaagccggtgttctctcttaagcagaaaagtctctgctcgaagtgctgcccggga	6501
Db	3905	TGAGGAGCTAGTACACGGCTTTGCCAGAAAAATTTGCAGAGTGTCTGCAGCGAGGCCAGA	3964
Qy	6502	ttgtgtcacacgaatacacagaagtgcttctgtcttctcaacttgacaacggaaagag	6561
Db	3965	GTGCGTCTCAAGCANTACAGAAATGTAATTTCCGACAACATAGACAACAGCCGCAC	4024
Qy	6562	accctctacgctacaccagatgaataaccaagctgagtgccgtgtatgccggagaagccat	6621
Db	4025	ACGACAAATTCACCCGCGATCATTTGAATGTGTGATTTCGTCCGTACGAGGTTACAAG	4084
Qy	6622	gcacacggccgggtgtgcacatctctacagagtttaagagagcagacatagccagtgac	6681
Db	4085	ACACGGAGTTGGAGCGGACCGCTGTAACCTGTAAGGGAGAACATTCGTGATTGTCA	4144
Qy	6682	agaaacgctgtgtttaacgcagctaacgccctgggaactgtaggggatggcgctatgcag	6741
Db	4145	AGAGGAACGATTTGTCAAATGCAAGCAATCCACTGGCGAGACCAGGAGAAGAGTCTGCCG	4204
Qy	6742	ggccgtggcgaagaaatggccgtcagcctttaagggaagcagaacacccagtgggcacaat	6801
Db	4205	TGCCATCTATAAAGCTTTGGCGGACAGTTTCACCGATTACGCCACACAGACAGTACCGC	4264
Qy	6802	taaaacagtcagtgcggcctgtaccgccgtcatccacgctgtagcccttaattctctgc	6861
Db	4265	AAAACTGACTGTGTGCCAAGAAAGAAAGTGATCCACGGGTGGCCCTGATTTCCGGAA	4324
Qy	6862	cacgactgaagcggaaagggacgcgaattggccgtgtctaccgggcagtgccgcgcga	6921
Db	4325	ACACCCAGAGCAGACCCCTGAAATGCTTGCAAAACGCCCTACCATGCACTGAGTGGCAGCTT	4384
Qy	6922	agtaacagagctgtcactgacgcgtgacctcccgcgtgcttcacagagtgagtgctcag	6981
Db	4385	AGTAAATTGAACATAATATAAGTCTGTCCCATCCCACCTGCTATCTACAGGCATTTCGC	4444
Qy	6982	cggcggaaagataggtcgcagcaatccctcaacatctattcacgcaatggagccac	7041
Db	4445	AGCGGAAAGACCCCTTAGGTATCACTTAACCTGCTTGACAAACCGCGCTAGACAGAAC	4504
Qy	7042	ggacgtgcgtgacatctactgcagacaaaaagttgggagaagaaaaatccaggaagc	7101
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Qy	7102	cattgacatggagcgggtgt---ggattgctcaatgatgactgagtgagctgacacaga	7158
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Qy	7159	cttggtgagatgacacccggacagcagcgtgggtgctgaaggctacagtaccactga	7218
Db	4625	GTTAGTATGGATCCATCCGACAGTTCCTGAAGGAAGAAGGGATTCAGTACTACAAA	4684
Qy	7219	cgggtcgtctactgtactttgaaggtacgaataatcaacaggctgctattgatggc	7278
Db	4685	AGGAAAGTTGATTTCGTACTTTGAAGGCACCAAAATTCATCAAGCAGCAAAAGATATGC	4744
Qy	7279	agadactgacgttgtggccagactgcgaagggcgaacgaacagatatgacctatcgc	7338
Db	4745	GGAGATAAAGTCTGTTCCCAATACGAGGAAGCAAGCAACAACTGTGTGCTTACAT	4804

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5885	Db	CCAGATGATGCCACCGGAAGCCACAAAACGAGGTACCGTCTCGAAAAGTAGAAAACCA	5944
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8359	Qy	agggcgcataccacacatcagcgggttcgggtaccccgcccggttactccccctaccgtgat	8418
6002	Db	AGATCAGCCAGGAATGCTATAGATCACTACCCGAACCACTCGTATTCCAGCAGTGTACC	6061
8419	Qy	cgaaagattctcaagcccgatgtagcaatcgagcgtgcaacagaaatacctatccagaaa	8478
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8479	Qy	ttaccacaagtggtgctctaccagaataacagatgaatacacgacatacttggacatgggt	8538
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8719	Qy	gcgagaaactaccacatgactcggcaggtgttcaacgtggagtgcttcaagcgctatgc	8778
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8779	Qy	ctgtctcggagaatattgggaagaatatgtbaaacaacttatccggataaacactgagaa	8838
6422	Db	ATGCAATGACGAGTATTGGGAGGAGTTTGGCCGAAAGCCAAATTAGGATCACTACTGAGTT	6481
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6542	Db	GCATAATTTGGTCCCATTTGCAAGAAGTGCCTATGATAGATTCTCATGGACATGMAAAG	6601
8959	Qy	agatgtcaaaagtcactccagggcgaacacacagaggaagaaagccaaagtcceaggtaat	9018
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Qy	9379	gtttctgacttgtttattaaacactgttttgaacatcaccatagcaacaggggtactggga	9438
Db	7022	GTTCCTCAGGCTCTTTGTCACACAGTCTTGATATGTCGTATATGCGCCACAGAGTATTGGA	7081
Qy	9439	gcagagactcactgaactccgcctgtgctggcccttcacgcgcacacacaacatcgttcacgg	9498
Db	7082	GGAGCGGCTTAAAAAGTCCAAATGTGCGACATTTATCGCGACGACACAATATACACGG	7141
Qy	9499	agtgatctccgcacaagctgatggcgagaggtgcgcgtcgctgggtcaacatggaggtgaa	9558
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Qy	9559	gactcagcgcctgctcatggcggaaccccccatatttttgggggattcatagtttt	9618
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Qy	9619	tgacagcgtccacacagacacgcctgcgcgtgtttcagaccacttaagcgcctgtcgaagt	9678
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Qy	9679	gggttaacgcctaaacagttaagacaacagcaggaagaagacagcgcagcagcactgagtga	9738
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Qy	9799	taggtatgaggttagaggcgtgcacaaagtatcctcatagccattgcccacttggcgagga	9858
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Qy	9859	cattaaggcgtttagaagaattgagagacctgttatcacaccttcacggctcctagatt	9918
Db	7502	CAAAAGAGCATTTCAAGCCATCAGAGGGGAAATAAGCATCTCTACGGTGGTCTCTAAATA	7561
Qy	9919	ggtgcgttaataca	9932
Db	7562	GTACGATAGTACAA	7575
RESULT	10		
Id	T47668		
Id	T47668	standard; cdna; 11663 bp.	
Ac	T47668;		
Dt	19-MAY-1997	(first entry)	
Dt	19-MAY-1997	(first entry)	
Kw	S.A.ARB6;	Sindbis virus; attenuation; vaccine; diagnosis; antibody;	
Kw	S.A.ARB6;	Sindbis virus; attenuation; vaccine; diagnosis; antibody;	
Os	vector; ockelbo;	polyarthritis; ss.	
Os	South African Arbovirus No. 86.		
Fh	Key	Location/Qualifiers	
Ft	mutation	215	
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Ft		/note= "a guanine for adenine substn. at nucleotide	
Ft		215 is a preferred silent mutation used in	
Ft		recombinant DNA constructs of the	
Ft	mutation	invention"	
Ft		3863	
Ft		/*tag= b	
Ft		/note= "a guanine for cytosine substn. at	
Ft		nucleotide 3863 is a preferred silent	
Ft		mutation used in recombinant DNA constructs	
Ft		of the invention"	
Ft	mutation	3984	
Ft		/*tag= c	
Ft		/note= "a guanine for adenine substn. at nucleotide	
Ft		5984 is a preferred silent mutation used in	
Ft		recombinant DNA constructs of the	
Ft		invention"	
Ft	mutation	9113	
Ft		/*tag= d	

	/note= "a cytosine for thymine substn. at nucleotide 9113 is a preferred silent mutation used in recombinant DNA constructs of the invention"
FT	WO9637220-A1.
PD	28-NOV-1996.
PF	U07457.
PR	22-MAY-1996; US-446932.
PA	(UYNC-) UNIV NORTH CAROLINA.
PI	Davis NL, Johnston RE, Simpson DA;
DR	WPI; 97-020937/02.
PT	New recombinant DNA encoding infectious South African Arbovirus 86 RNA transcript and related mutants - under control of heterologous promoter, useful in prodn. of attenuated vaccines and to generate diagnostic antibodies
PS	Claim 2; Page 13-19; 27pp; English.
CC	A cDNA clone (T47668) codes for an infectious South African Arbovirus No. 86 (S.A.AR86) virus RNA transcript. Novel recombinant DNA constructs comprise the cDNA, pref. mutated to include attenuating and silent mutations, and an upstream heterologous promoter (pref. T3, T7 or SP6). Infectious attenuated viral particles produced from cells transfected with the RNA transcripts encoded by such cDNA clones are useful in live attenuated vaccines, e.g. against diseases caused by related viruses such as Ockelbo, and can also be used as vectors to express antigens of other viruses. The cDNA clone can be administered to animals to raise antibodies for diagnosis of S.A.AR86 infection.
SQ	Sequence 11663 BP; 3297 A; 3104 C; 2903 G; 2359 T;
	Query March 14.5%; Score 2255.2; DB 1; Length 11663; Best Local Similarity 58.2%; Pred. No. 3.6e-261; Matches 4374; Conservative 0; Mismatches 2903; Indels 237; Gaps
QY	2644 agtscagtgtgatcaggccgacagcccattcatcaagtccttcgcagaaggaattcc 2703
Db	74 AGTTAAGCTAGCGTAGACCCCTCAGAGTCGGTTGTGTCGAACCTGCAAAGAGCTTCCC 133
QY	2704 gtccctcgagggtggagtgatcattgcaggtcacaccaaatgacctgcaaatgccagacatt 2763
Db	134 GCAAATTGAGGTAGTAGCACAGCAGGTCACTCCAATGACCATGCTANTGCCAGACATTT 193
QY	2764 ttccgacctggctaccaattgatcagcaggagactgacaaaagacacatactcttggaa 2823
Db	194 TTCGATCTGGCCAGTAACATACTCAGCTGGAGGTTCTTACCACAGCAGCATTTTGGAA 253
QY	2824 tatcggcagtcgccttcacgaggaatgatctcacgcacaataaccactggatgcccc 2883
Db	254 CATPAGCAGCGCACCGGTCGTAGAATGTTTTCCGAGCACCATACATTTGGTTTGCCCC 313
QY	2884 tatggcgacgcagaagaccocgaaggtctegatagctacgaagaagaactggcagcgcc 2943
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QY	2944 ctccgggaaggtgctggtagagagatcgcaggaaaaatacccgacctcagacacgtcat 3003
Db	374 AGCATGTAAAGATTACAACAAGRACTTGCATGAGAGATCAAGGACTCTCCGACCGTACT 433
QY	3004 ggctaagccagcagctgaattcactcacttttgcctgcatacagacgtcagctgctgtac 3063
Db	434 TGATACACCGGATGCGAAACGGCCATCATTCTGCTTCCACAACGATGTTACCTGCAACAC 493
QY	3064 ggcagccgaagtggccgttataccaggaagctgtatgctgtacatgcacacaatcgctgta 3123
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QY	3124 caatcagcgcatgaaggtgtcgaacgcttatggattggattggattggattggattggatt 3183
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QY	3184 tatgttgtcgcgtatgcagcgcgtatccaaccttaccccaactcgcacaaactcgcgcagagca 3243
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[illegible]

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QY	4795	cttg	gggttcc	gggata	cagcaag	ctgtct	tatt	taagag	ctcgtg	tacc	aaacac	ga	4854							
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QY	4855	tctg	ctcacc	agcg	caaga	ggagaa	ctgc	ccag	aaata	agtt	aaacac	tactag	tagagt	4794						
Db	2291	tctgtt	tacc	agcg	caaga	ggagaa	ctgc	ccag	aaata	agtt	aaacac	tactag	tagagt	4794						
QY	4915	ccg	gggaag	ggggac	agtag	ggaaac	agtg	actcc	atcctg	ctgt	aaac	gggtg	ctgctg	4974						
Db	2351	gagg	ggcatg	cagatc	acgtcg	agacac	agtg	actcc	atcctg	ctgt	aaac	gggtg	ctgctg	4974						
QY	4975	tgcc	gtgaca	ctctat	atgtg	gacag	ggctt	cgctt	gcac	ctcc	ctg	ctg	ctg	5034						
Db	2411	agcc	gtag	aaag	tgctgt	ttgtg	acga	agcgtt	ccgctg	ccac	cgag	gagac	tactt	2470						
QY	5035	cc	taattg	ctt	gttaa	acotc	ggag	caaa	agtg	gtgt	ttat	tcg	gagag	cccaag	5094					
Db	2471	cttg	atg	caat	tcg	acag	ccccc	gtc	at	aa	ggtag	tgct	atg	tcg	gagag	cccaag	5094			
QY	5095	cg	gattct	ccaata	tgatg	cagctt	aa	ggtag	tgct	atg	tcg	gagag	cccaag	5094						
Db	2531	cg	gattct	ccaata	tgatg	cagctt	aa	ggtag	tgct	atg	tcg	gagag	cccaag	5094						
QY	5146	ca	ctga	agt	atg	tcata	aaag	tata	tc	ccag	ctgt	gc	ag	ctgc	ag	cccaag	5094			
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QY	5206	gt	ctag	ttg	ctac	ta	cgag	ggca	agat	gc	gc	ac	ccca	cccg	tg	caac	aaac	cccaat	5265	
Db	2651	at	cg	acac	tc	gatt	ac	gatt	ac	gatt	ac	gatt	ac	gatt	ac	gatt	ac	gatt	ac	5265
QY	5266	ca	ta	ga	ca	ca	ca	ca	ca	ca	ca	ca	ca	ca	ca	ca	ca	ca	ca	5266
Db	2711	aat	cg	ac	at	ttac	ag	ggcc	ac	ga	ag	cc	ga	ag	cc	ga	ag	cc	ga	5266
QY	5326	ag	gt	gg	gca	aa	gag	ctg	ctg	gg	act	acc	gt	gg	ac	ca	ca	ca	ca	5326
Db	2771	cg	gt	gg	gca	aa	gag	ctg	ctg	gg	act	acc	gt	gg	ac	ca	ca	ca	ca	5326
QY	5385	at	ct	ga	gg	ct	ca	cc	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	5385
Db	2831	ct	ca	aa	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	5385
QY	5446	ct	gt	at	g	cc	ct	g	ct	g	ct	g	ct	g	ct	g	ct	g	ct	5446
Db	2891	g	ct	gt	at	g	cc	ct	g	ct	g	ct	g	ct	g	ct	g	ct	g	5446
QY	5506	ag	gt	gg	aaaa	ac	g	ct	g	ct	g	ct	g	ct	g	ct	g	ct	g	5506
Db	2951	ag	ta	tg																

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 Db 4085 AGACGGAGTTGGAGCGCACCTGATACCGCACTAAAGGGAGAACTATGTGATTGTCA 4144
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Db 4145 AGAGAAACGACGTTGTCAATGCAGCCAAATCCGCTGGGAGACACAGGCGAAGAGTCTGCCG 4204
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 Db 4205 TGCCATCTATAAAGCTTTGGCCGAACACTTTACCGATTACGCCACAGAGACCGGACCGC 4264
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 Db 4265 AAAACTGACTGTGTGCCCAAGAAAGATGATCCACGGGGTTGGCCCTGATTTCCGGAA 4324
 QY 6862 cagactgaagcgaaggggagccgcgaattggcgcgtgtctaccggcgagtgagcgacga 4384
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 Db 4805 ATTGGGGAGACCATGCAAGCAATCCCGAAAAATGCCCGTCGACCCACAAACCGCTGC 4864
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 QY 7459 ccgctttaggtcacacacagtttaaaagcagtggtggttctctatcttccctcccgaa 7518
 Db 4925 CAGACTCAGAAAGCAACNACGTCAGAAAGTTACAGTATCTCTCTCCACCCCTTCCAAA 4984
 QY 7519 ataccatgtatggtggtgcagaaggttaaagtgcgaaggttctcctgttcgacgcagac 7578
 Db 4985 GTACAAATCAGAAAGGTTTCAAGAGTTCAGTGCACAAAGTAGTCTCTTTAACCCGCA 5044
 QY 7579 ggtacctcagtggttagtcgaggaagtcgcgcatactacagcagcagcagcagctgc 7638
 Db 5045 TACCCCTGCTATTCGTCGCGCGTAAAGTACATAGAAGCGCCAGAACAGCCTGCACTCC 5104
 QY 7639 gtcgttacagaggt----- 7653
 Db 5105 GCCTGCACAGCGGAGAGGCCCCCGAAGTTGACAGCAACACCAACACCTGCAGCTGA 5164
 QY 7653 -----tgacttgactggaccacagcagctgc 7680
 Db 5165 TAACTCTGCTTGTATGTACGGACATCTACTTGACATATGAAGACAGTACGGAAGCTC 5224
 QY 7681 ttccactgcacagatcatgctgctaccagtttcagctcgtgtgaca-----tcgac 7735
 Db 5225 ACTCTTTTCAGCTTTAGCGGATCGGCAACTCTATTACTAGTATGGACAGATTGGTCTC 5284

[illegible]

Db 7442 AAAGCGTGGTTAGAGTAGGTATACAGACACCTTACGACGTGCCGTGCGCAACTCGGTA 7501
 Qy 9805 tgaggtagagggtgcacaaagatctcatcgatgccatggccaccccttgccagggagacattaa 9864
 Db 7502 TGAGGTAGAACACATCACACCTGTCTCTGCTGGCATTTAGAGACACTTTTGCCACAGCAAAAG 7561
 Qy 9865 ggcggttaagaattgagagacacctgttatcacactctacggcggtctctagattggtcg 9924
 Db 7562 AGCATTTCAAGCCATCAGAGGGGAAATAAGCATCTCTACGGTGGTCTCTAAATAGTCAGC 7621
 Qy 9925 ttaataca 9932
 Db 7622 ATAGCACA 7629

 RESULT 12
 V33476
 ID V33476 standard; cDNA; 11703 BP.
 V33476
 DE 10-DEC-1998 (first entry)
 DE Sindbis virus clone TR339 cDNA sequence.
 KW Bone marrow cell; alphavirus; sindbis virus; cytokine; capsid;
 KW reverse transcriptase-PCR; nsP1; nsP2; nsP3; nsP4; E3; E2; 6K; E1;
 KW growth hormone; growth factor; interleukin; chemokine; enzyme;
 KW ribozyme; antisense oligonucleotide; ss.
 KW Sindbis virus.
 KEY
 FEH Location/Qualifiers
 FT 5'UTR 1..59
 FT CDS /*tag= a
 FT 60..7601
 FT /*tag= b
 FT /product= "Non-structural polyprotein"
 FT /note= "Internal stop codon present at nucleotides
 CDS 7647..11384
 FT /*tag= c
 FT /product= "Structural polyprotein"
 FT 11382..11703
 FT /*tag= d
 W09836779-A2.
 27-AUG-1998.
 18-FEB-1998; U02945.
 19-FEB-1997; US-801263.
 (UYNC-) UNIV NORTH CAROLINA.
 Davis NL, Johnston RE, Simpson DA;
 WPI; 98-495361/42.
 P-PSDB; W70464, W70465, W70480, W70481, W70482, W70483, W70484;
 P-PSDB; W70485, W70486.
 Expression of heterologous RNA in bone marrow cells - using a
 recombinant alphavirus comprising a promoter operable in bone marrow
 cells operably associated with heterologous RNA.
 Example 6; Fig 6A-6B; 68pp; English.
 The invention provides a method for introducing and expressing
 heterologous RNA in bone marrow cells using alphavirus vectors.
 The present sequence represents the Sindbis virus clone TR339 cDNA
 polyproteins. The nonstructural polyprotein is, presumably,
 post-translationally modified into four different protein products,
 namely nsP1 (W70464), nsP2 (W70465), nsP3 (W70480), nsP4 (W70481)
 proteins. The structural polyprotein is, presumably, post-
 translationally modified into five different protein products, namely
 capsid (W70482), E3 (W70483), E2 (W70484), 6K (W70485), E1 (W70486),
 and 6K. The Sindbis virus cDNA was used in the method of the
 invention. The inventors claim the transformed bone marrow cells are
 useful for expressing a protein or peptide suitable for protecting the
 subject against a disease such as a microbial, bacterial, protozoal,
 parasitic or viral disease. The transformed bone marrow cells are also
 claimed to be useful for expressing proteins and peptides such as
 hormones, growth hormones, growth factors, interleukins, cytokines,
 chemokines, enzymes, ribozymes or antisense oligonucleotides.
 Sequence 11703 BP; 3306 A; 3051 C; 2913 G; 2433 T;

Query Match	14.3%	Score 2222.8	DB 1	Length 11703	
Best Local Similarity	58.4%	Pred. No. 2.6e-257			
Matches 4412	Conservative	0	Mismatches 2862	Indels 282	Gaps 19
QY 2644	agtcgctgtgtatctgagctgcagagccattcatcaagtccttgcagaagcgattcc	2703			
DB					
74	AGTAAACGTAGAGTAGACCCCGACAGTCCGTTGTGTGCAACTGCAGAAAGCITCCC	133			
QY 2704	gtcgttcgaggtggagtcattgcagaggtcacaccacaaatgaccattcaaatccagagcatt	2763			
DB					
134	GCAATTGTAGGTAGTACACAGCAGGTCACCTCCAAATGACCATGCTAATGCCAGACATT	193			
QY 2764	ttcgcacctggctaccaaattgatctgcagcaggagatcgcacaaagacacactcatcttga	2823			
DB					
194	TTCGCATCTGGCCAGTAAACTAATTCGAGCTGGAGTTCCTACCAAGCAGCATCTTGA	253			
QY 2824	tatcggcagtcgccttcaggagaaatgatctagcacaacataccactggtatgcgc	2883			
DB					
254	CATAGGCAGCGACCGGCTCGTAGAATGTTTCGGAGCACCATATCATGTGTGTGCC	313			
QY 2884	tatcgcagcagcagaagcccccgaaagtcgatctacgcacaaagaaactggcagcgcc	2943			
DB					
314	CATCGGTAGTCCAGAAACCCGACCCCATGATGAATATGCCAGTAACTGCCGGA	373			
QY 2944	ctccgggaagtgctgatatagagatcgcagagaaataccgcacctgcagacgctcat	3003			
DB					
374	AGCGTGAAGATTACAACACAGAACTTGATGATGAGAATTAAGGATCTCCGACCGTACT	433			
QY 3004	ggctacgccagaagctgaatctcctacctttgctgcatacagacgicacgctgcgtac	3063			
DB					
434	TGATACCCGGATGCTGAACACAACTATCGCTGCTTTTCAACAGATGTACTCGACACT	493			
QY 3064	ggcagcgcaagtgggcgtatcacagacagctgatctgtacatgcaccaacatcgtctga	3123			
DB					
494	CGGTGCCAATATTCCGTATCGAGACGTGTA---TATCAACGGTCCCGGAATATCTA	550			
QY 3124	ccatcagcgcatgaagggtgcagaacggcgtattggtattgggtttgcacacccccgt	3183			
DB					
551	TCATCAGGCTATGAAGGGCTCGGACCGCTGACTGATGGATTGGCTTCGACACACCCAGTT	610			
QY 3184	tatgtttgacgcctagcagcgctatccaaacctacgccacaaactgggcccagcagca	3243			
DB					
611	CATGTTCTCGGCTATGGCAGGTCTGACCTCGGTACCAACACCAACTGGGCCGACGAGA	670			
QY 3244	gggttacaggccaggaacataggactgtgtcagcataccttgactgagggagactcgg	3303			
DB					
671	AGTCTTGAAGCGCTAACTCGGACTTGCAGCACAAAGCTGAGTGAAGGTAGGACAGG	730			
QY 3304	caaatctgcattctccccaagaagcaattgaaaccttgcacacagtcgtttctcgt	3363			
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731	AAAATGTGTAATGAGGAGAGAGGAGTTGAAGCCGGGTGCGGGGTTTATTTCCTCGT	790			
QY 3364	aggatctacattgtacactgagacgaaagactactgaggagctgcacacttaacctcgt	3423			
DB					
791	AGGATCGACACTTATTCAGAAACACAGACCGACGCTTCCAGAGTGGCATCTTCATCGGT	850			
QY 3424	attccacctgaaggttaaacatcttacctgtagggtgcataccatcgtatcgtga	3483			
DB					
851	GTTCCACTGTAATGAAAGCAGTCTGACATTCGCCGTGTGTATACAGTAGTGTGAGTTGCCA	910			
QY 3484	agggtaactagtttaagaaaatcaatatgtgccccggcctgcaggttaaacaggttaggta	3543			
DB					
911	AGGCTACGTAGTGAAGAAATCACCATCATCGTCCCGGGATCACGGGAAACCGTGGGATA	970			
QY 3544	cgcggtgacgtatcacgvggagggattccttagtgtgcagaaccacagacactgtcaagg	3603			
DB					
971	CGCGGTTACACAATAGCAGGAGGCTCTGTGTATGCAAGTTACTGACACAGTAAAGG	1030			
QY 3604	agaaagagttcattccctgtatgaccctcagctccctcaaccatctgtgatcaaatgac	3663			
DB					
1031	AGAACGGGTATCGTTCCTGTGTGSCAGTATACATCCGGGCCCATCATGCGATCATGATGAC	1090			

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Db	2171	AGCTCTGGAGGGACTGAGAGCCCGACCTCGGTCCCGTACAAGGTGCAAAACAATAGAGT	2230
Qy	4795	ctttggggttccgggattcaaggcaagctctgtattattaaagcctctgtgaccaaacacga	4854
Db	2231	GATAGGCACACGGGGTGGGCAAGTCAGCTATTATCAAGTCACTGTCACGGCACGGGA	2290
Qy	4855	tctgttcaacgcgcgaagaagagagaactgccagggaatagttaacgacgtgnaagca	4914
Db	2291	TCTTTGTTACCAAGCGGAAGAAGAAATGTCGCGAAATTGAGCGCGACGTGCTAAGACT	2350
Qy	4915	ccgcgggaagggaagaagtgggaacaacagtgactccatcctctaaacgggtgfcgctg	4974
Db	2351	GAGGGGTATGCAGATTACGTCGAAACAGTAGAATTCGGTTATGTCTCAACGATGCCACAA	2410
Qy	4975	tgccgtggacatcctatgttgagcagggttttcgcttgccattccggtactctgtgctg	5034
Db	2411	AGCCGTFAGAGTGTCTGTACGTTGACGGAAGCTTCGGGTGCGGTGCCACGAGGACACTATTGC	2470
Qy	5035	cctaattgctcttggtaaacctcggagcaagtggtgtttatgcgagaccccaagaatg	5094
Db	2471	CTTGATGTGCTATCGTCAGGCCCGCCAGAGAAGGTAGTACTATGCGGAGACCCCATGCATG	2530
Qy	5095	cggattctcaatatgatgcagcttaaggtgaactccaacc-----aacatctg	5145
Db	2531	CGGATTCTTCAACATGATGCACTAAAGGTACATTCAATCACCTGAAAAGACATATG	2590
Qy	5146	cactgaagtatgtcatanaagtatatccagacgttgacggtccaggtccagtcgcccctgt	5205
Db	2591	CACCAAGACATTTACAAGTATATCTCCGGCGTTGCACAGCGGCTACACTATTGT	2650
Qy	5206	gtctaacttgactacgaggaagaatgctgcagcaccaaccgtgcaacaaacccataat	5265
Db	2651	ATCGACACTGCATTACGATGGAAGATGAAMACCAGCAACCGGTCAAGAAGAACATTTGA	2710
Qy	5266	catagacaccacggagcagcaagcccaagccagagacatcgtttaacatgcttcg	5325
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Qy	5326	agctggggcaagcagctcagttgactaccgtggacacgaagtcatgacagcagcagc	5385
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Qy	5386	atctcaggctccaccgcgaagggtgatacgcgtgaaggcagaagtggaatgaatcc	5445
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Qy	5446	cttgtatgccctgctcgagacatgaaatgactgctgaacgcgactgaggaatagct	5505
Db	2891	ACTGTACCGCATACATCAGACATGTGAACGTGTGCTCACCGCACTGAGGACAGGCT	2950
Qy	5506	ggttggaaaaacgctggccggcgatccctggatgaaggctctatacaacattccacagg	5565
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Qy	5566	taactttaagccacattggaagaatggcaagaacacgacaaataatgaaggtgat	5625
Db	3011	AAACTTTCAGGCTACTATAGAGGACTGGGAAGCTGACACAAAGGAATAATTCGTGCAAT	3070
Qy	5626	tgaaggacggctgctgcctgtggacgcttcagaaacaaagaaacgctgtgtgggcga	5685
Db	3071	AAACGCCCCACTCCCGCTGCCAATCCGCTCAGCTGCAAGACCAACGTTGCTGGCGGAA	3130
Qy	5686	aagccttgggtgctgtccttgacactgcgaatacagattgacagcagagagtgagacac	5745
Db	3131	AGCATTTGGAACCGATACTAGCCACGGCCGGPATCTACTTACCGGTTGCCAGTGGACGA	3190
Qy	5746	cataattacagcatttaaggagacagagcttactctccagttggccttgaaatgaat	5805
Db	3191	ACTGTTCCACAGTTTTCGGATGACAAACCAACATTCGGCCATTTACGCCCTTACAGCTAAT	3250
Qy	5806	ttgacccaagctactatggagttgacctgacagctggcctgtttctgcccccaaggtgct	5865

3251 TTGCATTAAAGTTTTTCGGCATGGACTTTGACAAGCGGACTCTTTTCTAAACAGAGCATCC 3310

5866 cctgtattacagaaac-----cactgggataaacagacactgg 5904

3311 ACTAACGTACCATCCCGCGGATTACGAGCGCGGTAGTCTATTGGGACAAACAGCCAGG 3370

5905 tggaaagatgtatgattcaatccgcaacagctgcagcgtcggaagctagacatacatt 5964

3371 AACCCGCAAGTATGGTACGATCACGCCATTGCGCGCAACTCTCCGTGATATTCGGGT 3430

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RESULT 13

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Q86154
AC Q86154 standard; DNA; 16656 bp.
ID Q86154;
DT 21-NOV-1995 (first entry)
DE Eukaryotic layered vector initiation system derived from Sindbis.
KW Eukaryotic layered vector initiation system; Sindbis; alphavirus;
KW transcription initiation; non-structural protein; subgenomic fragment;
KW RNA polymerase recognition sequence; ELVIS; gene therapy; ss.
OS Sindbis virus.
FH Key
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FT FT /product= NSP1, NSP2, NSP3 polyprotein
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FT FT /*tag= c
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FT FT /*tag= d
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FT FT /*tag= e
FT FT /bound_moeity= Sindbis polymerase
FO WO9507994-A.
PD 23-MAR-1995.
PF 15-SEP-1994; U10469.
PR 15-SEP-1993; US-122791.
PR 18-FEB-1994; US-198450.
PA (VIAG-) VIAGENE INC.
PI Chang SWW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;
PI Polo JM;
PT WPI: 95-131362/17.
PT New alpha virus vectors for gene therapy - of viral infection,
PT cancer, auto-immune disease, etc., and as vaccines.
PS Disclosure: Fig 3: 260pp; English.
SC This sequence represents a eukaryotic layered vector initiation
CC system (ELVIS) derived from Sindbis. This sequence comprises a'
CC sequence capable of initiating transcription of an alphavirus, a
CC nucleotide sequence encoding alphavirus non-structural proteins, a
CC viral junction region which has been inactivated such that viral
CC transcription of the subgenomic fragment is prevented, and an
CC alphavirus RNA polymerase recognition sequence. Inactivation of the
CC viral junction region prevents transcription of the subgenomic
CC fragment making vectors such as this suitable for a wide variety of
CC applications, eg. gene therapy.
SQ Sequence 16656 BP; 4468 A; 4349 C; 4183 G; 3656 T;

Query Match 14.2%; Score 2211.6; DB 1; Length 16656;
Best Local Similarity 58.3%; Pred. No. 5.2e-256;
Matches 4405; Conservative 0; Mismatches 2869; Indels 282; Gaps 1

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OY 2884 tatcgcagcgcagaaagacccccgaaggctcgcgatgctacacaagaactcgcagcggc 2943
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Db 4382 CTTAGTAATGAACATTAACATCAAGTGTGCGCCATTTCCACTGCTATCTACAGCAATTTA 4441
QY 6979 cagcggcgaagagataggtcagac 7038
Db 4442 CGCAGCGGAAAGACCGCTTGAAGTATCACCTAACCTGCTTACAAACCGCTTACCATGATGAG 4501
QY 7039 cagcagcgtgactgaccatctactgacagacacacacacacacacacacacacacacacacac 7098
Db 4502 AACTGACCGGACCTACCATCTATTGCTGGATAGAGAGTGAAGAAAGAAATGACACG 4561
QY 7099 agccattgacatgagcagcgtgt---ggagttgctcaatgatgacgtgagcgtgacac 7155
Db 4562 GGCACCTCAACTTAAAGAGTCTGTACAGAGCTGAAGAGTGAAGATGAAGATGAAGATGAAGAT 7215
QY 7156 agacttggtagagtgacacccgac 7275
Db 4622 TGAGTTAGTAGTATGCATCCACACAGTTGCTTGAAGGAGAAAGAGGATTTCAGTACTAC 4681
QY 7216 tgacgggtgctgactgtacttgaaggtacgaaattcaaccggcgtgctattgat 7275
Db 4682 AAAGGAAATTTGATTCGTACTTCGAGGACCAAAATTCATCAAGCAGCAAAAGACAT 4741

QY 7276 ggcagagactgacgt 7335
Db 4742 GCGGAGATAAAGTCTGTTCCTTAATGACCAAGAAAGTAAATGAACAACTGTGTGCTTA 4801
QY 7336 cgcgcgt 7395
Db 4802 CATATGGGTGAGACCATGGAAGCAATCCGGAAGAGTCCCGGTGACCAATACCCGTC 4861
QY 7396 atcaacacactccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 7455
Db 4862 GTCTAGCCCGCCCAACGTTGCGTTCCTTGTGATGTATGCTATGCTATGCTATGCTATGCT 4921
QY 7456 cgcgcgt 7515
Db 4922 CCACAGACTTTAGAAAGCAATAACGTCAAAGAAAGTACAGTATGCTCTCCACCCCGCTTCC 4981
QY 7516 gaaatacactgttagatgggggtgcagaaggttaagtgtagaaggtttctctctgtgtgtgtgt 7575
Db 4982 TAAGCACAAATTAAGAAATGTTTCAGAAAGGTTCAGTGCAGGAAAGTAGTCTCTTTAATCC 5041
QY 7576 gacgggtaccttcagttgt 7635
Db 5042 GCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAAGTGCAGAAACACCTTACC 5101
QY 7636 tccgt 7692
Db 5102 TCTCTCTGACAGCGCGAGAGGCCCGCCGAAAGTTGTAGCGACACCGTCCACCATCTACAGC 5161
QY 7693 cgatacactgt 7734
Db 5162 TGATACACCTCGCTGTATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAGG 5221
QY 7735 ctgatgt 7781
Db 5222 CTCACCTTTTTCGAGCTTTAGCGGATCGACAACTCTATTACTAGTATGAGACAGTTGGTC 5281
QY 7782 accctgaaccccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 7839
Db 5282 GTCAGGACCTAGTTCACATAGATAGTAGAGCAAGCAAGCAGGTGTGTGTGTGTGTGTGTGT 5341
QY 7840 caatgtgacctcagaaac 7899
Db 5342 TGCCGTCCATAGCTGCGCCCTATTCACACCGCAAGGCTAAAGAAAGATGCGCCGCTGGC 5401
QY 7900 ctcccgccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 7930
Db 5402 ACGGCAAGAAAGAGGCCACTCCACCGCAAGCAATAGCTCTGAGTCCCTCCACCTCTC 5461
QY 7930 -----gcgagaaagccgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 7951
Db 5462 TTTTGGTGGGTATCCATGTCCCTCGCATCAATTTTCGACGGAGAGACGGCCCGCCAGGC 5521
QY 7952 ccaagactcgttttagaacaagc-----tgcctttgacgttctcgagcagcagcagcagcagc 8001
Db 5522 AGCGGTACACCCCTGCAACAGCGCCCGCAGGATGTGCTATGTCTTCGGATCGTTTC 5581
QY 8002 cgaacagaggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 8054
Db 5582 CGACGGAGAGATTGATGAGCTGAGCGCAGCACTGAGTCCGAACCGCTCTCTTTGG 5641
QY 8054 ----- 8054
Db 5642 ATCATTTGAACCGGGGAAAGTGAATTAATATATGCTCCCGATCAGCGGTATCTTTTCC 5701
QY 8054 -----gacgtctgcgactagcagcagcagcagcagcagcagcagcagcagcagcagcagc 8076
Db 5702 ACTACGCAACGACAGCAGTAGACGCAAGGAGAGGAGTGAATTAATGACTAATCCGGGT 5761
QY 8077 ggtgcatattttctcctcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 8136
Db 5762 AGTGGGTACATATTTTCGACGACACAGCCCTGGGCACCTGGCACCTTGCANAAAGAGTCCGTCT 5821

QY	8137	gcagcacaatctccagttcgccacaactgagtcggtccaggagagagaaattgtaccgcgc	8136
DB	5822	gcagAACCAAGCTTACAGAACCGACCTTGGAGCGCAATGTCTCTGGAAGAATTCATGCGCC	5881
QY	8197	aaattggatactgagaggagaaagctgtgtgctgtaaaatgcagatgcagatcccatcgga	8256
DB	5882	GGTGTCTGACAGCTCGAAGAGAGCAACTCAAACTCAGGTACCAAGATGATGCCACCGA	5941
QY	8257	ggctaaataagatcgataccagctctcgaaaagtggagaaatgaagccagcagtggtgga	8316
DB	5942	AGCCAAACAAAGTATGAGTACACAGTCTCGTAAGATGAGAAATCAGAAAGCCATAAACCACTGA	6001
QY	8317	caggctcacatcgggggccagattgtacacggagcggagcgtaggccgcgcataccacaata	8376
DB	6002	GCACACTGTGAGGACTACGACTGTATA---ACTGTGCACAGATACGCCAGAATGCTA	6058
QY	8377	cgcggttcggtgaaccccgccccgtgtactccctaccgtgatcgaaagattctcaagccc	8436
DB	6059	TAAGATCACCTATCCGAACCAATGTACTCCATACGTTACCGCGCACTACTCCGATCC	6118
QY	8437	cgatgtagaatcgacgcgtgcacgaatacctatccagaataccccaacagtggcgc	8496
DB	6119	ACAGTTGCTGTACGTCTGTAAACAACTATCTGCATGAGAACTATCCGCACAGTAGCATC	6178
QY	8497	gtaccagataacagataatacagcgcatacttgacgcatacttgacgcgttcgagatggtg	8556
DB	6179	TTATCAGATTACTGACGAGTACGATGTCTTCTTGATATGTTAGACGGGACAGTCCGCTG	6238
QY	8557	cttgacagagcgacattctgcgcggcggaagctccggtgctacccgaacacatacgcgt	8616
DB	6239	CCTGGATACTGCACCTCTGCCCCGTAAAGTTAGAAAGTACCGAAAAAATAGTAGTA	6298
QY	8617	ccaccagcgcactgtacgcagtcgcgtcccgctcaccctttcaaacacactacagaacgt	8676
DB	6299	TAGACCCCGCAATATCCGACGTGCGGTTCATCAGCGATGCGAAGAACGCTACAAATGT	6358
QY	8677	gctagcgcgcaccacaagagaaactgcacgcgtcacgcnaatgcgcagaactacccacat	8736
DB	6359	GGCTAATGCCCGCACTAAAGAAATTCACGTCACGCAGATGCGTGAACCTGCCAACACT	6418
QY	8737	ggactcgcgcagttctcaacgtggagtgcttcaagcgtatccgtcctccggagaaattg	8796
DB	6419	GGACTCAGCGACATTCATGTGCAATGCTTCGAAATATGCAATGTAATGACGAGTATG	6478
QY	8797	ggaagaatatgcataaacacctatccggataaccactgagaacatcactatcctatgac	8856
DB	6479	GAGAGATTCGCTCGGAACCCAAATTAGGATTACCCTGAGTTGTTCACCGCATATGAC	6538
QY	8857	caaatgaaaggccgcgaagctgtgcctgttctcctaagaccacacacttggctccgct	8916
DB	6539	TAGACTGTAAAGGCCCTTAAGGCCCGCACACTATTTGCAAGACGCTATTAATTTGGTCCCAT	6598
QY	8917	gcaggaggttccatggacagattccacggtcgacatgaacgcagatgtccaagtcaactcc	8976
DB	6599	GCAAGAAGTCCCTATGGAATAGATTCTGATGACATGAAAGAGACGCTGAAAGTTTACACC	6658
QY	8977	agggaagaaacacacagaggaagaagcccaagtcaggttaattcaagcagcggagccatt	9036
DB	6659	AGGCACGAAACACACAGAAAGAACGCGAAGTACAAAGTATACAAAGCCGACAGACCCCT	6718
QY	9037	ggcagcgtctactgtgcgggcattccacaggggaattagtaaggagagactaaatgcgtgct	9096
DB	6719	GGGACATGCTTACTTATGCGGGATTCACCGGAATTAGTGTGCGTACGCTTACGCGCGCTCT	6778
QY	9097	acgccttaacgctgocacatatgtttgaatatgtcggccgaagacattgcgcgatcagc	9156
DB	6779	GCTTCCAAACATTCACACGCTTTTGTGATGTGCGGCGAGGATTTTGTATGCAATCAGC	6838
QY	9157	ctctcatctccaccagagaccgggtcttagagacggacattgcattcatcttagacaaaag	9216
DB	6839	AGAACACTTCAAGCAAGCGACCCGGTACTGGAGACGGATATCGCATCAITTCACAAAAAG	6898
QY	9217	ccaggacgcactccttgctcttaacagtttaatgatacctcgagatcctaggggtggata	9276

6899	CCAAGACGCGCTATGGCGTTAAACCGGTCGTATGATCTTTGAGAGACCTGGGTGGGATCA	6958
9277	gtactctgagactgaatcagagcagcctttgggaaatatccagctgtcacctaccaac	9336
6959	ACCACTACTCGACTTGTATCGAGTGGCCCTTTGGAGAAATATCATCCACCCATCTACCTAC	7018
9337	tggcacgcgctcaagtctcgagactatgatgaatcggcactgtttctcgaattgtttat	9396
7019	GGGTACTGCTTTAAATTCGGGGCGATGATGAATCCGGAATGTTCTTCACACATTTTGT	7078
9397	taacactgttttgaaatacaatacaacagcagggctactggagcagagactcaactgactc	9456
7079	CAACACAGACTTTTGAATTCGCTTATCGCCACGAGACTACTAGAAAGCGGCTTAAACGTC	7138
9457	cgctgtgcgcttcactcgcgacgacaaacatcgttccagcgagtgatctcgcacaagct	9516
7139	CAGATGTCGCGGTCATTGTCGCGACGACAAATCATACATGATGAGTAGTAGTGTGACAAAGA	7198
9517	gatggcgagaggtgcgcgtcgtaggttcaactggagggtgaagatcattgacgctgtcat	9576
7199	AATGGCTGAGAGGTGCGGCACCTCGCTCAACATGGAGGTTAAGATCATCGACGATCAI	7258
9577	ggcgaaaaccccccatattttgtggggattcatagttttgacagcgctcacacagac	9636
7259	CGGTGAGACACACCTTACTTCTGCGGGATTTATCTTCAAGATTCGTTACTTCCAC	7318
9637	cgctgcgctgtttcagaccacactaagcgcctgttcaacttgggttaacgcgtacacgc	9696
7319	AGCGTCCCGCTGGCGGGATCCCTGAAAGGCTGTTTAAGTTGGGTAAACCGCTCCACG	7378
9697	tgaagacaagcagcgacgaagacagcgcagcagcactgagtgacgaggttagcaagtggtt	9756
7379	CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG	7438
9757	ccggcagcaggttggggcgcaactgaggtgagcactaacatctagttatgagtagaggg	9816
7439	TAGAGTAGGTATAAACAGGACACTTTAGCAGTGGCGCTGACGACCGGTATGAGGTAGACAA	7498
9817	ctgcaaaagtatcctcactagccatggccactcttggcaggagacattgaagcggtttaagaa	9876
7499	TATTACACCTGTCTCTACTGGCATTCAGACACTTTGCCAGAGCAAAAGAGCATTTCCAAGC	7558
9877	attgagaggacctgttatcacctctacggcgctcactagattggtcggttaataca	9932
7559	CATCAGAGGGGAAATAAAGCATCTACGGTGGCTCTAAATAGTCAGCATAGTACA	7614
RESULT	14	
T30787		
ID	T30787 standard; DNA; 16656 BP.	
AC	T30787;	
DT	12-SEP-1996 (first entry)	
DE	Alphavirus-based eukaryotic layered vector pVGLVLS.	
KW	Alphavirus; Sindbis virus; vector; gene therapy; vaccine;	
OS	pVGLVLS; ss.	
OS	Chimeric Sindbis virus;	
OS	Chimeric synthetic.	
FH	Key	
FT	Location/Qualifiers	
FT	promoter	1..60
FT	/tag= a	
FT	/note= "wild-type Sindbis virus sequence-	
FT	capable of initiating transcription"	
FT	60..5750	
FT	/tag= b	
FT	/product= non-structural proteins NSP 1-3	
FT	5928..7579	
FT	/tag= c	
FT	/product= non-structural protein NSP 4	
FT	7579..7602	
FT	/tag= d	
FT	/function= minimal junction region core	
FT	11647..11703	
FT	misc_feature	

RESULT 14

T30787	standard; DNA; 16656 BP.
AC	T30787; 1996 (first entry)
DE	12-SEP-1996 (first entry)
DD	Alphavirus-based eukaryotic layered vector pVGELVIS.
DE	Alphavirus; Sindbis virus; vector; gene therapy; vaccine;
KW	pVGELVIS: ss.
KW	pVGELVIS: ss.
OS	Chimeric Sindbis virus;
OS	Chimeric synthetic.
OS	Chimeric synthetic.
FFH	Location/Qualifiers
FFH	1..60
FT	promoter
FT	/*tag= a
FT	/note= "wild-type Sindbis virus sequence
FT	capable of initiating transcription"
FT	60..5750
FT	cds
FT	/*tag= b
FT	/product= non-structural proteins NSP 1-3
FT	5928..7579
FT	cds
FT	/*tag= c
FT	/product= non-structural protein NSP 4
FT	7579..7602
FT	misc_feature
FT	/*tag= d
FT	/function= minimal junction region core
FT	11647..11703
FT	misc_feature

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FT      /*tag= e
FT      /function= sindbis polymerase recognition
FT      sequence
PN      WO9617072-A2.
PD      06-JUN-1996.
PR      30-NOV-1995: U15490.
PR      30-NOV-1994: US-348472.
PR      18-JAN-1995: US-376184.
PR      15-MAR-1995: US-405827.
PA      (CHIR ) CHIRON VIAGENE INC.
PI      Belli BJ, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;
PI      Jolly DJ, Polo JM;
PI      WPI: 96-277785/28;
PT      New recombinant alpha-virus vectors - used to develop prods and
PT      methods for use in gene therapy and in the prodn. of vaccines
PS      Example 2; Page 186-194; 256pp; English.
CC      A eukaryotic layered vector initiation system, pVGE1VIS (730787),
CC      is based on the Sindbis alphavirus. It is obtd. by inserting
CC      the Sindbis clone pVSP6GENrep into vector pCDNA3. The construct
CC      can be used in the prodn. of Sindbis virus-based vectors used
CC      to develop products and methods for use in gene therapy and in
CC      vaccine prodn. pVGE1VIS is capable of initiating alphavirus
CC      infection; inactivation of the viral junction region (see also
CC      730810) will prevent viral transcription of the subgenomic
CC      fragment. The efficiency of pVGE1VIS in generating wild-type
CC      Sindbis virus after transfection of BHK cells was approx. 1,000
CC      pfu/mg plasmid DNA.
SQ      Sequence 16656 BP: 4469 A; 4352 C; 4179 G; 3656 T;

Query Match      14.2%; Score 2211.6; DB 1; Length 16656;
Best Local Similarity 58.3%; Pred. No. 5.2e-256;
Matches 4405; Conservative 0; Mismatches 2869; Indels 282; Gaps 19;

QY      2644  agtgcattgtattgaggtcagacccattcatcaagttcttgcagaaagcatttcc 2703
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      74  AGTAACGATAGAGTACAGCCCGAGTCCGTTTCGTGCAACTGCAAAAGGCCCTCCC 133
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      2704  gtcgttcgaggtggagtcattcaggtcacacaaatgacacatgacaaatgccagagcatt 2763
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      134  GCAATTTGAGGTAGTAGACACACAGCTGCTCTCCAATGACCATGCAATGCGAGCAATT 193
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      2764  ttccgacctggctacaaattgatcagcagagactgacaaagacacacacatcattctgga 2823
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      194  TTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGTCTCTACCAAGCAGCATCTTGGGA 253
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      2824  tatcgccagtgcgcttcagagaaatgatctctacgcacaaataccactcgtatgcc 2883
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      254  CATAGCAGCGCACCCTGCTAGTAATGTTTTCGAGCACCAGTATCATGTCCTGCC 313
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      2884  tatcgccagcagaaagaccgaaagctcgatagctacgcacaaatccacgacctgcagccgtcat 3003
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      314  CATCGTAGTCCAGAAAGACCCGCGCATGATCAATATGCCAGTAACTGCGGAGAAA 373
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      2944  ctccgggaagtgctggatagagatgcgcaggaataatccacgacctgcagccgtcat 3003
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      374  ACCGTGCAGATTTACAACAAGAACTTGCATGAGAGAAATTAAGGATCTCCGGACCGTACT 433
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3004  ggctacgacagcgtgaaatctctactcttggctcgcacacagagctcagctgctgtac 3063
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      434  TGATACGCCGATGCTGAACACCATCGCTCTGCTTTTCACAAAGATGTTACCTGCAACAT 493
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3064  ggacgccaagtggcgtataccaggagctgtatgctgtacatgcaccacaacatcgctgta 3123
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      494  CGGTGCCGAATATTCCTGTCATGAGGAGCGTGA---TATCAACGCTCCCGGAATATCTA 550
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3124  ccattcagcgtgaaaggtgtcagaacggtgattgattggtgttgacacacacccgtt 3183
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      551  TCATCAGGCTATGAAGGCGTGGACCCCTGTACTGATGCTTCGACACACACCCAGTT 610
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3184  tatgtttgacgctagcagcgcgtatccaacctacgcacacaaactggccgacagca 3243
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      611  CATGTTCTCGGCTATGCGCAGGTTTCGTACCTGGGTACACACCACTGGGCCGACGAGAA 670
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY      3244  ggtgttacagccaggaacatagagactgtgtgcagcatctcttgactagggaaactcgg 3303
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      671  AGTCCTTTGAAGCGCGTAACATCGGACTTTGCGACACAAAGCTGAGTGAAGTAGGACAGG 730
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3304  caaactgtccattctccgcaagaagaacttgaacacttgcacacagctcattgttctcgtt 3363
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      731  AAAATTGTGCGATAATGAGGAAGAGGAGTTGAACCCCGGCTGCGGGTTTATTTCCTCCGT 790
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3364  aggatctacattgtacactgagagcagaagaactactgagagctggtgacacttacccctcgt 3423
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      791  AGGATTCGACATTTATCCAGAACACAGAGCGAGCTTGCAGAGCTGGCATCTTCATCGGT 850
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3424  attccacctgaaggttaacaactcttacccttagtgcgataccatcgtatcattgtga 3483
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      851  GTTCCACTTGAATGGAAGCAGTCGTACACTTCCCGCTGTGATACAGTGTGAGTTGCGGA 910
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3484  aggtacgtgttaagaaatcactatgtgccccgcctgtacggttaaaacggttaggta 3543
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      911  AGGCTAGCTAGTGAAGAAATACCATCAGTCCCGGATCACGGGAGAAACCGTGGGATA 970
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3544  cgccgtgacgtatcacgcgagagattcctagtgtcaagaccacacagacactgtcaaaagg 3603
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      971  CGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAAGTTACTGACACAGTAAAGG 1030
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1031  AGAACGGGTATCGTTCCTTGTGTGACGTACATCCCGGCCACCATATGGATTCAGATGAC 1090
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3664  tggcactactagcagccgctcacaccggagagcagcagaagttgttagtgggattgaa 3723
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1091  TGTCTTANTGGCCACCGATATATCACCCTGACGATGCACAAAACCTCTCTGTTGGCTCAA 1150
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3724  tcagagtagttgtgaacggaagacacagcgaaactaacactaacacagcagatgaagaactatct 3793
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1151  CCAGCGAATGTCATTAACGGTAGGACTTAACAGGAACACCAACACCATGTCAAAATACCT 1210
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3784  gcttcgagattgtggcgcgtgcatttagcaagtggcgagggaatacaaggcagacacctga 3843
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1211  TCTGCCGATCATAGCACAAAGGGTTTCAGCAAAATGGGCTAAGGAGCGCAAGGATGATCTGA 1270
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3844  tgatgaaaaaccttgggtgtccgagagaggttcacttacttctgctgctgttgggcaatt 3903
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1271  TAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGCTGTGCTGTGGGGGTT 1330
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3904  taaacgagggaagtgcacacacatgtacaagaacacagacacccacagacaaatagtgaaggt 3963
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1331  TCGCACTAAGAAAGTACATTCGTTTATCGCCCACTTGAACGCGCAGACCTGCGTAAAGT 1390
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      3964  gcttcagagtttaactcgttcgtccatcccgagcgtatgtctacagggcctcgaatccc 4023
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1391  CCCACGCTTWTAGCGGTTTCCCACTGTGCTCGTATGAGCAGACCTCTTTGCCATGTC 1450
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      4024  agtcagatcacgcattaaagtgtctttggccaagaagacacacagcgagagtaataacctgt 4083
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1451  GCTGAGGCAGAAAATGAAACTGGCATTGCAACCAAGAGAGGAGAAAACCTGCTGAGGT 1510
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      4084  tctcgaagcgt-----cgtcagccagggatgctgaacaagagagagagaggttga 4137
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1511  CTCGGAGGAATTAGTCATGAGGCCCAAGGCTGCTTTTGGAGATGCTCAGGAGGAAGCCAG 1570
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      4138  ggccgagtagctagagaagccttaccacccctcgtcccc---catcgccgcgcgcgcgcgcgc 4194
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1571  AGCGGAGAAGCTCGAGAACACACTTCCACCATAGTGGGACAGAAAGGATCATGAGGACAGC 1630
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      4195  ggaggtcgtcagagtgagcgtgaagaactagatgtatcagcaggtgtcaggggtgtgtga 4254
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1631  CGCAGAAGTTGTCTGGCAAGTGGAGGGGGTCCAGGCGGACATCGGAGCAGCATAGTTAGA 1690
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      4255  aacacctcgcagcgcgtgtgaagctcaccgcacagcgcagcagcgtactactactaggaatta 4314
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1691  AACCCCGCGGGTCACGTAAAGGTAATACCTCAAGCAATGACCGTATGATCGGACAGTA 1750
DB      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 4315 cgtagttctcccgagaccggtgctcaagagctccaaagttggcccccggtgcacacctct 4374
 Db 1751 TATCGGTGTCTCCCAAACTCTGTGAGAAATGCAAACTCGCAGCAGCCACCCGCT 1810
 QY 4375 agcagagcaggtgaaataataacacataacagggagggcgccggttaccaggtgcacgg 4434
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 QY 4435 atagcagcaggttccctactaccatgctgagtcgcatccggtccctgagtttcaagc 4494
 Db 1871 ATACGACGCTAAAGTACTGATGCCAGCAGGAGTGCCTACCATGCCAGAAATTCCTAGC 1930
 QY 4495 tttagcgagagcgccactatggtacacagaaagggagtttgcacacagaaactata 4554
 Db 1931 ACTGAGTGAGAGCCACGTTAGTGTACAAAGAAAGAGATTGTGAACGCCAACTATA 1990
 QY 4555 ccatttgcggttccagcagcgtcgctgaacacgcagcagaggaactacagaaagtcag 4614
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RESULT 15
 V42364
 ID V42364 standard; DNA; 16556 BP.
 AC V42364;
 DT 02-OCT-1998 (first entry)
 DE Representative eukaryotic layered vector initiation system sequence.
 KW DNA alphavirus; structural protein expression; inhibit; pathogen;
 immune response; stimulate; ss.
 OS Sindbis virus.
 PN US789245-A.
 PD 04-AUG-1998.
 PF 30-OCT-1996; 741881.
 PR 15-MAR-1995; US-404796.
 PR 15-SEP-1993; US-122791.
 PR 18-FEB-1994; US-198450.
 PR 30-NOV-1994; US-348472.
 PR 20-JAN-1995; US-376184.
 PR 30-OCT-1996; US-741881.
 PI (CHTR) CHIRON CORP.
 PA Chang SWW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ,
 PI Polo JM;
 DR WPI: 98-446089/38.
 PT DNA alpha-virus structural protein expression cassettes - for
 PT producing recombinant alpha-virus particles
 PS Disclosure; Fig 3A-H; 140pp: English.
 CC The present sequence is a representative eukaryotic layered vector
 CC initiation system derived from Sindbis virus. The specification describes
 CC a DNA alphavirus structural protein expression cassette which comprises
 CC an inducible promoter and an alphavirus structural protein gene, where
 CC the promoter directs the expression of the alphavirus structural protein
 CC gene upon induction of the promoter within a cell, and where prior to
 CC induction within the cell, the expression cassette does not express
 CC sufficient quantities of structural proteins to be cytotoxic to a BHK
 CC cell containing the expression cassette. The products may be used to
 CC inhibit pathogens and stimulate an immune response.
 SQ Sequence 16556 BP; 4467 A; 4349 C; 4183 G; 3657 T;

Query Match 14.2%; Score 2211.6; DB 1; Length 16556;
 Best Local Similarity 58.3%; Pred. No. 5.2e-256;
 Matches 4405; Conservative 0; Mismatches 2869; Indels 282; Gaps 19;
 QY 2644 agtcgatgttgataggcgtacagcccatcctaagctctttgcagaagcgatttcc 2703

Query Match 14.2%; Score 2211.6; DB 1; Length 16656;
Best Local Similarity 58.3%; Pred. NO. 5.2e-256;
Matches 4405; Conservative 0; Mismatches 2869; Indels 282; Gaps 19;
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|||||

[illegible][illegible]

Db 4442 CCGACCGCGAAAGACCGCCCTTGTAAGTATACATCTTAAGTCTTGACAACCGCGCTAGACAG 4501
 QY 7039 cccgagcgtgacgtgaccatctactgcagagacaaagttggagagaaatccaggga 7098
 Db 4502 AACTGACCGGACGTAACACTCTATTGCTGGATAAGAGTGAAGAAAGATCGACGC 4561
 QY 7099 agccattgacatgagcagcggctgt---ggagtgtcctaatgtagcagcgtgagctgaccac 7155
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 QY 7156 agacttggtagagtcgaccctggagacagccctgggtggtcgtgaaggctacagtcaccac 7215
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 QY 7216 tgacgggtcgtgactcgtacttgaagtagcagaatacaacagcgtgctatgat 7275
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 QY 8857 caaatgaaagcccgaaagctgctgcttgccttaagccccacacacttggctccgct 8916
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Sun Feb 13 13:44:46 2000

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QY	8981	AGGCACGAACACACAGAGAAAGACCCGAAAGTACAAGTATACAAGCGCAGAAACCCCT	6718
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DB	8984		
QY	8985	GGCGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGGGTAGGCTTACGGCGGCTTT	6778
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QY	9009	CAACACAGATTTTGAATGTCTTATCGCCACGAGACTAGTAAGAGCGGCTTAAACGTC	7138
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QY	9011	cgcctgtcgcgcttcacgtcgcgacacacatcgttccagcgagtgtatccgcacagct	9516
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QY	9013	CAGATGTGCAGCGTCAITTGGCGAGCAACATCATACATGAGTAGTAGTATCTGACAAAGA	7198
DB	9014		
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QY	9017	AATGGCTTGAAGAGTGGCGCACCTGGCTCAACATGGAGGTTTAAATCATCGACGCGATCAT	7258
DB	9018		
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QY	9021	CGGTGAGAGACCACTTACTTCTGGCGGGATTTATCTTGCAGATTCGGTACTTCCAC	7318
DB	9022		
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DB	9028		
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DB	9042		

Search completed: February 9, 2000, 05:39:30
Job time: 2795 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2000, 07:45:53 ; Search time 9215.41 Seconds
(without alignments)
-5119.613 Million cell updates/sec

Title: US-09-190-246-1

Perfect score: 15538

Sequence: 1 tcgcgcgttcgtgatgac.....tatcaagagcccttcgtc 15538

Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmbl : *

Word size : 0

Number of hits that pass the threshold : 1642386

1: gb_ba1:*
2: gb_ba2:*
3: gb_ov:*
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50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7399.2	47.6	11517	5	A18788	A18788 complete nu
2	7399.2	47.6	11517	5	AR001293	AR001293 Sequence
3	7392.8	47.6	11442	16	ALSFV42S	X01129 Semliki for
4	7336.6	47.2	7422	16	SF0251359	AJ251359 Semliki F
5	7168.6	46.1	7746	16	SFVRNALS	Z48163 Semliki for
6	3917.6	25.2	4093	16	SFV11207	Y17207 Semliki For
7	3144	20.2	11657	16	RRVNBGG	M20162 Ross River
8	2967.2	19.1	5900	5	AR064320	AR064320 Sequence
9	2967.2	19.1	5952	5	AR064321	AR064321 Sequence
10	2964	19.1	5676	5	AR064322	AR064322 Sequence
11	2964	19.1	5682	5	AR064323	AR064323 Sequence
12	2911.8	18.7	11835	16	ONNGC	M20303 O'Nyong-nyo
13	2908.4	18.7	11821	16	AF079457	AF079457 Igbo Ora
14	2894	18.6	11822	16	AF079456	AF079456 O'nyong-n
15	2520.6	16.2	11488	16	BFU73745	U73745 Barmah Fore
16	2272.8	14.6	11663	5	AR042409	AR042409 Sequence
17	2272.8	14.6	11663	5	I46902	I46902 Sequence 1
18	2272.8	14.6	11663	16	ACU38305	U38305 Sindbis-lik
19	2271.2	14.6	11663	5	AR042411	AR042411 Sequence
20	2266	14.6	11344	16	AF075256	AF075256 Venezuela
21	2234.4	14.3	11717	5	AR042410	AR042410 Sequence
22	2224.4	14.3	11717	16	ACU38304	U38304 Sindbis-lik
23	2223.4	14.3	11385	16	AF075259	AF075259 Venezuela
24	2223	14.3	11311	16	AF075255	AF075255 Venezuela
25	2222.8	14.3	11703	5	AR042412	AR042412 Sequence
26	2216.4	14.3	11703	16	SINCG	J02363 Sindbis vir
27	2215.4	14.3	11717	16	AF103734	AF103734 Sindbis-1
28	2211.6	14.2	16856	5	AR020969	AR020969 Sequence
29	2211.6	14.2	16856	5	AR043384	AR043384 Sequence
30	2211.6	14.2	16856	5	AR062299	AR062299 Sequence
31	2208	14.2	11626	16	AF103728	AF103728 Sindbis v
32	2183	14.0	11824	16	SINOCK82	AF136284 Aura viru
33	2179	14.0	11708	16	SINOCK82	M69205 Ockelbo vir
34	2170.8	14.0	11391	16	AF075253	AF075253 Venezuela
35	2167	13.9	11420	16	AF004472	AF004472 Venezuela
36	2163.8	13.9	11420	16	AF004458	AF004458 Venezuela
37	2157.4	13.9	11420	16	AF004459	AF004459 Venezuela
38	2157.4	13.9	11420	16	VEU55360	U55360 Venezuelan
39	2156.8	13.9	11395	16	AF075251	AF075251 Venezuela
40	2154.2	13.9	11421	16	AF100566	AF100566 Venezuela
41	2152.4	13.9	11441	16	VEU55382	AF075251 Venezuela
42	2146.6	13.8	11422	16	EEVNSPECFA	AF100566 Venezuela
43	2135.4	13.7	11444	16	EEVNSPECFA	U55362 Venezuelan
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ALIGNMENTS

RESULT 1
LOCUS A18788
DEFINITION complete nucleotide sequence of PSP6-SFV4 RNA transcript.
ACCESSION A18788
VERSION A18788.1
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 11517)
AUTHORS

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Qy	7228	gtactgtactttgaaggttacgaattcaaccaggtgctattgatattggcagagatact	7287
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Qy	7288	gagttgtgcccagactgcaagaggcaaacgacagagatatgctatacgcgtggcgga	7347
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Qy	7348	aaatggaacacatcagatccaaatgcccgtgaacgattccgattcatcaacacatcc	7407
Db	4802	AACAAATGGACAAACATCAGATCCAAATGTCGGTGAACGATTCCGATTATCAACACGCTCC	4861
Qy	7408	caggacagtgccctgctgtccgctacgaaatgacagcagaaggtatgccgccttag	7467
Db	4862	CAGGACAGTGCCCTGCTGTGCCCTACGCAATGACAGCAGAGGATGCGCCCTTAG	4921
Qy	7468	gtcacacaatttaaaagcatggtgtgtctcatctttccctcccgaataaccatgt	7527
Db	4922	GTCAACACAAGTTAAACGATGGTGTGTCTCATCTTTTCCCTCCCGAAATACCATGT	4981
Qy	7528	agatgggtgcagaaggttaaagtcgagaaggttctctgttcgacccgacggtaccctc	7587
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Qy	7588	agtggttagtcgcggaagtatgcgcctctacgacgagaccactcagatcggtcgttacg	7647
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VERSION X04129.1 GI:58614
KEYWORDS capsid protein; genome; nonstructural protein; polyprotein; structural protein; Semliki Forest virus.
SOURCE Semliki Forest virus.
ORGANISM Semliki Forest virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus.
REFERENCE 1 (bases 1 to 7520)
AUTHORS Takkinen,K.
TITLE Complete nucleotide sequence of the nonstructural protein genes of Semliki Forest virus
JOURNAL Nucleic Acids Res. 14 (14), 5667-5682 (1986)
MEDLINE 86286581
REFERENCE 2 (bases 7121 to 7480)
AUTHORS Riedel,H., Lehrach,H. and Garoff,H.
TITLE Nucleotide sequence at the junction between the nonstructural and the structural genes of the Semliki forest virus genome
J. Virol. 42 (2), 725-729 (1982)
REFERENCE 3 (bases 7387 to 8335)
AUTHORS Garoff,H., Frischauf,A.M., Simons,K., Lehrach,H. and Dellius,H.
TITLE The capsid protein of Semliki Forest virus has clusters of basic amino acids and prolines in its amino-terminal region
Proc. Natl. Acad. Sci. U.S.A. 77 (11), 6376-6380 (1980)
REFERENCE 4 (bases 8212 to 11442)
AUTHORS Garoff,H., Frischauf,A.M., Simons,K., Lehrach,H. and Dellius,H.
TITLE Nucleotide sequence of cdna coding for Semliki Forest virus membrane glycoproteins
Nature 288 (5788), 236-241 (1980)
JOURNAL 81052444
COMMENT Data kindly reviewed (23-MAR-1987) by K. Takkinen.
FEATURES
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Sun Feb 13 13:44:44 2000

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QY	9508	cgacaagctgatggcgagaggtgcgctgctgggttcaacatggaggtgaagatcattga	9567
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QY	9868	gtttaagaataatgaggagacctgtataccctctacggcggtccttagattcggtcgta	9927
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	SOURCE	Semliki Forest virus.			
	ORGANISM	Semliki Forest virus. Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;			

REFERENCE AUTHORS	TITLE	JOURNAL
1 (bases 1 to 7422) Tuittila, M. T., Santagati, M. G., Roeyttae, M., Maeaettae, J. A. and Hinkkanen, A. E.	Replicase complex genes of Semliki Forest virus confer lethal neurovirulence	Unpublished

Unpublished
2 (bases 1 to 7422)
Tuittila, M.T.
Direct Submission
Submitted (30-NOV-1999) Tuittila M.T., Department of Biochemistry
and Pharmacy, Abo Akademi University, Tykistokatu 6A, 20520 Turku,
FINLAND

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Sun Feb 13 13:44:44 2000

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VERSION	Z48163.1	GI:663260	
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AUTHORS	Tarbutt,C.J. and Atkins,G.J.		
TITLE	The complete sequence of the Semliki Forest virus strain A7		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 7746)		
AUTHORS	Tarbutt,C.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-FEB-1995) Catherine J Tarbutt BSc., Microbiology, The		
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 VERSION
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 ORGANISM
 Semliki Forest virus.
 Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 Alphavirus.
 REFERENCE
 1 (bases 1 to 4093)
 Tuittila,M.T., Santagati,M.G., Roytta,M., Maatta,J.A. and
 Hinkkanen,A.E.
 TITLE
 Prototype Semliki Forest virus nsp3/nsp4 gene region expressed by
 avirulent SFV47(74) confers lethal neurovirulence
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 4093)
 Hinkkanen,A.E.
 TITLE
 Direct Submision
 JOURNAL
 Submitted (28-APR-1998) A.E. Hinkkanen, Abo Akademi University,
 Dept Biochemistry and Pharmacy, Biocity, Tykistökatu 6 A, 20520
 Turku, FINLAND

Sun Feb 13 13:44:44 2000

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RESULT

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DEFINITION	AR064321				
ACCESSION	AR064321				
VERSION	AR064321.1	GI:5993629			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 5952)				
	Huebner, R.C., Norman, J.A., Liang, X., Carner, K.R., Barbour, A.G. a				
	Luke, C.J.				
TITLE	Compositions and methods for administering Borrelia DNA				
JOURNAL	Patent: US 5846946-A 2 08-DEC-1998;				
FEATURES	Location/Qualifiers				
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source	/organism="unknown"				

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Qy	14887	gaatcagatattcttctaataacctgaatgctgtttcccggggacgcagtggtgagt	14946
Db	5057	GAATCAGGATATTCTCTAATACCTGGAACTGCTTTCCGGGGATCGCAGTGTGAGT	5116
Qy	14947	aacctgcattcatcaggagtagcgataaaatgcttgatggtcggaagaggcataattcc	15006
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LOCUS AR064322 5676 bp DNA PAT 29-SEP-1999			
DEFINITION Sequence 3 from patent US 5846946.			
ACCESSION AR064322			
VERSION AR064322.1 GI:5993630			
KEYWORDS			
SOURCE Unknown.			
ORGANISM Unknown.			
Unclassified.			

REFERENCE	1 (bases 1 to 5676)									
AUTHORS	Huebner,R.C., Norman,J.A., Liang,X., Carner,K.R., Barbour,A.G. and Luke,C.J.									
TITLE	Compositions and methods for administering Borrelia DNA									
JOURNAL	Patent: US 5846946-A 3 08-DEC-1998;									
FEATURES	Location/Qualifiers									
source	1..5676									
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ORIGIN	/organism="unknown"									
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Best Local Similarity	99.6%; Pred. No. 0;									
Matches 2981; Conservative	0; Mismatches 10; Indels 1; Gaps 1;									
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QY	12608	cttcttgacctggaagtgccactcccactgctcttctctataataaaatgaggaattg	12667							
Db	2501	CTTCTTGACCTGGAAGTGCCACTCCCACTGCTCTTCTTAATAAATGAGGAATTG	2560							
QY	12668	catcgattgtctgagtagtgcttcttcttctggtggtggtggtggtggtggtggtg	12727							
Db	2561	CATCGCAATTGCTGAGTAGTGTGTCATTCTATTTCTGGGGGTGGGTGGGACACAGCA	2620							
QY	12728	agsgggagagattgggaagacaatagcagcagatgctggggatgctgggtctatgggta	12787							
Db	2621	AGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGGA	2680							
QY	12788	ccaggtgctgaagaattgacctggttccctctggtggtggtggtggtggtggtggtg	12847							
Db	2681	CCCAGGTGCTGAAGAAATGACCCGGTTCCTCTGGCCAGAAAGAACAGGACACATCCC	2740							
QY	12848	ttctctgacacacacctgtccacgcccctggttctttagttccagcccactcataggac	12907							
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Db	3041	CGGCTGCGGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGTTTATCCACAGATCA	3100							
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Db	3101	GGGGATACCGAGAAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGCAAAAGCCGTA	3160							
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RESULT 11
AR064323

LOCUS AR064323 5682 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5846946.
ACCESSION AR064323
VERSION AR064323.1 GI:5993631
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5682)
AUTHORS Huebner,R.C., Norman,J.A., Liang,X., Carner,K.R., Barbour,A.G. and Luke,C.J.
TITLE Compositions and methods for administering Borrelia DNA
JOURNAL Patent: US 5846946-A 4 08-DEC-1998;
FEATURES Location/Qualifiers
source l. 5682
BASE COUNT 1524 a 1358 c 1351 g 1449 t
ORIGIN
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Best Local Similarity 99.6%; Pred. No. 0;
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QY	14827	acaggaaatcgaatgcaaccggcgaggaacacgccagcgcatcaacaatatatttcaact	14886
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 O'Nyong-nyong virus (Gulu strain) complete genome.
 M20303.1 GI:32558
 nonstructural protein; polyprotein.
 O'Nyong-nyong virus (strain Gulu, isolated from Anopheles gambiae),
 cDNA to viral RNA, clones 2,4,7,8,9,11,13,14,17,17s,18,22,23,27,
 passed in BHK-21 cells.
 O'nyong-nyong virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 Alphaviruses.
 1 (bases 4079 to 7621)
 Strauss,E.G., Levinson,R., Rice,C.M., Dalrymple,J. and Strauss,J.H.
 Nonstructural proteins nsP3 and nsP4 of Ross River and
 O'Nyong-nyong viruses: Sequence and comparison with those of other
 alphaviruses
 Virology 164, 265-274 (1988)
 88206074
 2 (bases 1 to 11835)
 Levinson,R.S., Strauss,J.H. and Strauss,E.G.
 Complete sequence of the genomic RNA of O'Nyong-nyong virus and its
 use in the construction of alphavirus phylogenetic trees
 Virology 175, 110-123 (1990)

FEATURES	source
mRNA	
CDS	

Location/Qualifiers

1. .11835
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DITVSEGVYKRVVMTSPGIVGYKTSYAVTHYAGGFLMCKTTDVGERSYFSCVTV
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QY	7318	cgaaacagatatcctatagcgcgtggcgaaacaataatgacacacatcagatcccaattgcc	7377
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Db	5599	ATTGTATCACCAACCACTTACCCTCGAACCGGATCACTTTCGGAGACATTCGCCGAAGGTGAAT	5658
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REFERENCE
AUTHORS Lanciotti, R.S., Ludwig, M.L., Rvauma, E.B., Lutwama, J.J., Kram, T.M.,
Karabatsos, N., Cropp, B.C. and Miller, B.R.
TITLE Emergence of epidemic O'nyong-nyong fever in Uganda after a 35-year
absence: genetic characterization of the virus
JOURNAL Virology 252 (1), 258-268 (1998)
MEDLINE 99092493
REFERENCE
AUTHORS Lanciotti, R.S., Ludwig, M.L., Rvanuma, E.B., Lutwama, J.J., Kram, T.M.,
Karabatsos, N., Cropp, B.C. and Miller, B.R.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1998) Division of Vector-Borne Diseases, Centers
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